

GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.  
OM protein - protein search, using sw model  
Run on: March 28, 2006, 20:19:53 ; Search time 188 Seconds  
(without alignments)  
624.011 Million cell updates/sec

Title: US-09-803-918A-2  
Perfect score: 1362  
Sequence: 1 MKA AVLTLAVLFLTG SQARH.....SFKVSFLSALEEYTKKLNTQ 267

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_21:\*  
1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*  
9: geneseqp2005s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1362	100.0	267	1 AAP61079	Aap61079 Assumed h
2	1362	100.0	267	1 AAP82128	Aap82128 Entire hu
3	1362	100.0	267	2 AAR72705	Aar72705 Human apo
4	1362	100.0	267	2 AAR34032	Aar34032 Sequence
5	1362	100.0	267	2 AAY18675	Aay18675 Human apo
6	1362	100.0	267	4 AAB47620	Aab47620 Full leng
7	1362	100.0	267	5 AAO15892	Aao15892 Human apo
8	1362	100.0	267	5 ABG97593	Abg97593 Human apo
9	1362	100.0	267	6 ABR44031	Abr44031 Human apo
10	1362	100.0	267	6 ABP57065	Abp57065 Human apo
11	1362	100.0	267	6 ADA61214	Ada61214 Human apo
12	1362	100.0	267	7 ADJ83084	Adj83084 Human apo
13	1362	100.0	267	8 ADI19752	Adi19752 Human APO
14	1362	100.0	267	8 ABM81308	Abm81308 Tumour-as
15	1362	100.0	267	9 ADY75146	Ady75146 Brain tum
16	1362	100.0	267	9 AEA17397	Aea17397 Human pro
17	1362	100.0	267	9 AEA81148	Aea81148 Human apo
18	1362	100.0	267	9 AEB43205	Aeb43205 Human apo
19	1362	100.0	275	6 AAO30162	Aao30162 Human APO
20	1359	99.8	267	7 ADJ68447	Adj68447 Human hea
21	1359	99.8	267	7 ADJ83083	Adj83083 Human pro
22	1355	99.5	267	6 ABR44032	Abr44032 Human mut
23	1354	99.4	267	2 AAW08602	Aaw08602 Human apo
24	1351.5	99.2	268	1 AAP80668	Aap80668 Recombina

25	1346	98.8	267	8 ADE76862	Ade76862 Human pro
26	1328	97.5	299	4 AAU33170	Aau33170 Novel hum
27	1306	95.9	267	7 ADJ83086	Adj83086 Apolipopr
28	1306	95.9	267	9 AEA17413	Aea17413 Crab-eati
29	1306	95.9	267	9 AEA17418	Aea17418 Olive bab
30	1299	95.4	267	7 ADJ83087	Adj83087 Crab-eati
31	1286	94.4	276	9 AEA17594	Aea17594 Apolipopr
32	1286	94.4	518	9 AEA17555	Aea17555 Apolipopr
33	1286	94.4	518	9 AEA17565	Aea17565 Apolipopr
34	1285	94.3	524	9 AEA17598	Aea17598 Apolipopr
35	1285	94.3	526	9 AEA17602	Aea17602 Apolipopr
36	1285	94.3	528	9 AEA17607	Aea17607 Apolipopr
37	1285	94.3	530	9 AEA17611	Aea17611 Apolipopr
38	1284	94.3	462	9 AEA17589	Aea17589 Apolipopr
39	1284	94.3	562	9 AEA17616	Aea17616 Apolipopr
40	1284	94.3	566	9 AEA17624	Aea17624 Apolipopr
41	1282	94.1	424	9 AEA17576	Aea17576 Apolipopr
42	1282	94.1	666	9 AEA17551	Aea17551 Apolipopr
43	1281	94.1	249	7 ADJ83085	Adj83085 Human pro
44	1281	94.1	251	9 AEA17571	Aea17571 Apolipopr
45	1281	94.1	464	9 AEA17580	Aea17580 Apolipopr

ALIGNMENTS

RESULT 1  
AAP61079  
ID AAP61079 standard; protein; 267 AA.  
XX  
AC AAP61079;  
XX  
DT 25-MAR-2003 (revised)  
DT 07-OCT-1991 (first entry)  
XX  
DE Assumed human apolipoprotein A-1 derivative gene product.  
XX  
KW Hyperlipaemia; arteriosclerosis.  
XX  
OS Homo sapiens.  
XX  
PN JP61096998-A.  
XX  
PD 15-MAY-1986.  
XX  
PF 16-OCT-1984; 84JP-00216988.  
XX  
PR 16-OCT-1984; 84JP-00216988.  
XX  
(MITU ) MITSUBISHI CHEM IND LTD.  
XX  
DR WPI; 1986-165025/26.  
DR N-PSDB; AAN60886.  
XX  
PT Human apo:lipoprotein A-1 (deriv.) prepn. - by providing DNA fragment in  
PT cloning site downstream of expression vector promoter and introducing  
PT into host microorganism.  
XX  
PS Disclosure; Fig 2; 9pp; Japanese.  
XX  
CC The human apolipoprotein may be produced by a suitable transformed host,  
CC it is effective in treating hyperlipaemia and arteriosclerosis. (Updated  
CC on 25-MAR-2003 to correct PA field.)  
XX  
SQ Sequence 267 AA;

Query Match 100.0%; Score 1362; DB 1; Length 267;  
Best Local Similarity 100.0%; Pred. No. 3.7e-99;  
Matches 267; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MKA AVLTLAVLFLTG SQARHFQQDEPPQSPWDRVKDLATVYVDVLKDSGRDYSQFEGS 60  
Db 1 MKA AVLTLAVLFLTG SQARHFQQDEPPQSPWDRVKDLATVYVDVLKDSGRDYSQFEGS 60

QY 61 ALGKQLNLKLLDNWDSVTSTFSKLRQLGPVTQEFWDNLEKETEGLRQEMSKDLEEVKAK 120  
Db 61 ALGKQLNLKLLDNWDSVTSTFSKLRQLGPVTQEFWDNLEKETEGLRQEMSKDLEEVKAK 120  
QY 121 VQPYLDDFQKKWQOEEMELYRQKVEPLRAELQEGARQKLHELQEKLSPLGEEMRDRARAHV 180  
Db 121 VQPYLDDFQKKWQOEEMELYRQKVEPLRAELQEGARQKLHELQEKLSPLGEEMRDRARAHV 180  
QY 181 DALRTHLAPYSDELQRQLAARLEALKENGCGARLAEYHAKATEHLSTLSEKAKPALEDLRQ 240  
Db 181 DALRTHLAPYSDELQRQLAARLEALKENGCGARLAEYHAKATEHLSTLSEKAKPALEDLRQ 240  
QY 241 GLLPVLESFKVSFLSALEEYTKKLNQ 267  
Db 241 GLLPVLESFKVSFLSALEEYTKKLNQ 267  
RESULT 2  
AAP82128  
ID AAP82128 standard; protein; 267 AA.  
XX AAP82128;  
XX 25-MAR-2003 (revised)  
DT 24-OCT-1990 (first entry)  
XX Entire human preproapoprotein A1.  
DE human preproapoprotein A1; high density lipoprotein deficiency; ss.  
XX Synthetic.  
XX Key Location/Qualifiers  
FH Peptide 1. .18  
FT Peptide /label= precursor  
FT Peptide 19. .24  
FT Peptide /label= propeptide  
FT Protein 25. .267  
FT /label= mature apoprotein  
XX EP293357-A.  
PN  
XX  
PD 30-NOV-1988.  
XX  
PF 24-MAY-1988; 88EP-00870095.  
XX  
PR 28-MAY-1987; 87GB-00012540.  
XX  
PA (UNIO ) UCB SA.  
PA (BOLL/) BOLLEN A.  
XX  
PI Bollen A, Gobert J, Wulfert E;  
XX WPI; 1988-339891/48.  
DR N-PSDB; AAN82064.  
XX  
PT New DNA encoding human pro-apo-lipoprotein A1 - modified to eliminate  
PT hairpin structures.  
XX  
PS Disclosure; Page ?; 25pp; French.  
XX  
CC The cDNA 878bp fragment encoding preproapoprotein A1 was detected in  
CC clone pULB1609 derived from human liver cells. See also AAN81258.  
CC (Updated on 25-MAR-2003 to correct PA field.)  
XX  
SQ Sequence 267 AA;  
Query Match 100.0%; Score 1362; DB 1; Length 267;  
Best Local Similarity 100.0%; Pred. No. 3.7e-99;  
Matches 267; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MKA AVLTLAVLFLTG SQARHFQQDEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGS 60

Db 1 MKA AVLTLAVLFLTG SQARHFQQDEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGS 60  
QY 61 ALGKQLNLKLLDNWDSVTSTFSKLRQLGPVTQEFWDNLEKETEGLRQEMSKDLEEVKAK 120  
Db 61 ALGKQLNLKLLDNWDSVTSTFSKLRQLGPVTQEFWDNLEKETEGLRQEMSKDLEEVKAK 120  
QY 121 VQPYLDDFQKKWQOEEMELYRQKVEPLRAELQEGARQKLHELQEKLSPLGEEMRDRARAHV 180  
Db 121 VQPYLDDFQKKWQOEEMELYRQKVEPLRAELQEGARQKLHELQEKLSPLGEEMRDRARAHV 180  
QY 181 DALRTHLAPYSDELQRQLAARLEALKENGCGARLAEYHAKATEHLSTLSEKAKPALEDLRQ 240  
Db 181 DALRTHLAPYSDELQRQLAARLEALKENGCGARLAEYHAKATEHLSTLSEKAKPALEDLRQ 240  
QY 241 GLLPVLESFKVSFLSALEEYTKKLNQ 267  
Db 241 GLLPVLESFKVSFLSALEEYTKKLNQ 267  
RESULT 3  
AAR72705  
ID AAR72705 standard; protein; 267 AA.  
XX AAR72705;  
AC AAR72705;  
XX 31-OCT-1995 (first entry)  
DT Human apo A-I including signal and propeptide sequences.  
XX Apo A-I; LDL cholesterol; low density lipoprotein; lipid.  
XX Homo sapiens.  
XX Key Location/Qualifiers  
FH Peptide 1. .18  
FT Peptide /label= presignal  
FT Peptide 19. .240  
FT /label= claimed  
FT /note= "as part of fusion polypeptide"  
FT Peptide 19. .24  
FT /label= propeptide  
FT Peptide 120. .135  
FT /label= claimed  
FT /note= "as part of fusion polypeptide"  
XX US5408038-A.  
PN  
XX 18-APR-1995.  
PD  
XX 08-OCT-1992; 92US-00959946.  
PF  
XX 09-OCT-1991; 91US-00774633.  
PR 18-JUN-1992; 92US-00901706.  
XX  
PA (SCRI ) SCRIPPS RES INST.  
XX  
PI Witztum JL, Koduri KR, Young SG, Smith RS, Curtiss LK;  
XX WPI; 1993-134378/16.  
DR N-PSDB; AAQ89634.  
DR  
XX Polypeptide mimic of native apo B-100 and native apo A-I - useful in  
PT assays for LDL and HDL in plasma samples.  
PT  
XX Claim 10; Fig 2; 41pp; English.  
PS  
XX AAA89634 and AAR72705 depict the AA sequence of human apo A-I and its  
CC corresp. cDNA, including presignal residues and propeptide residues,  
CC according to Seilhamer et al., DNA 3(4):309 (1984). A dispersible apo A-  
CC I/B-100 fusion polypeptide is claimed which contains a first AA sequence  
CC of apo A-I and that includes at least AA sequence positions 120-135 (see  
CC AAR72606) and which reacts with pan anti-apo AI antibodies such as: AI-4

CC	ATCC HB8744; AI-7 ATCC HB 8745; AI-9 ATCC HB 8741; AI-10 ATCC HB 9200; AI-11 ATCC HB 9201; AI-12 ATCC HB 9202; AI-13 ATCC HB 9203; AI-14 ATCC HB 9204; AI-18 ATCC HB 9507
XX	
SQ	Sequence 267 AA;
	Query Match 100.0%; Score 1362; DB 2; Length 267;
	Best Local Similarity 100.0%; Pred. No. 3.7e-99;
	Matches 267; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 MKA AVLTLAVFLTGSQARHFQQDEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGS 60
DB	1 MKA AVLTLAVFLTGSQARHFQQDEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGS 60
QY	61 ALGKQLNLKLLDNWDSVTSTFSKLRQLGPVTQEFWDNLEKTEGLRQEMSKOLEEVKAK 120
DB	61 ALGKQLNLKLLDNWDSVTSTFSKLRQLGPVTQEFWDNLEKTEGLRQEMSKOLEEVKAK 120
QY	121 VQPYLDDFQKKWQEEMLYRQKVEPLRAELQEGARQKLHELQEKLSPLGEEMRDRARAHV 180
DB	121 VQPYLDDFQKKWQEEMLYRQKVEPLRAELQEGARQKLHELQEKLSPLGEEMRDRARAHV 180
QY	181 DALRTHLAPYSDELRLQRLAARLEALKENG GARLA EYHAKATEHLSTLSEKAKPALEDLRQ 240
DB	181 DALRTHLAPYSDELRLQRLAARLEALKENG GARLA EYHAKATEHLSTLSEKAKPALEDLRQ 240
QY	241 GLLPVLESFKVSFLSAL EYTKKLNTQ 267
DB	241 GLLPVLESFKVSFLSAL EYTKKLNTQ 267

CC claimed are a fusion polypeptide that contains: (a) a first amino  
CC acid residue sequence up to 250 residues in length that includes residues  
CC 120-135 of apo A-I, (b) a second amino acid residue sequence up to 375  
CC residues in length that includes residues 217-297 of apo B-100 and DNA  
CC encoding it. (Updated on 25-MAR-2003 to correct PN field.) (Updated on 25  
CC -MAR-2003 to correct PR field.)  
XX  
SQ Sequence 267 AA;

	Query Match	100.0%;	Score 1362;	DB 2;	Length 267;
	Best Local Similarity	100.0%;	Pred. No. 3.7e-99;		
	Matches 267;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0
QY	1	MKAAVLTLAVFLTGSQARHFQQDEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGS	60		
Db	1	MKAAVLTLAVFLTGSQARHFQQDEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGS	60		
QY	61	ALGKQLNLKLLDNWDSVTSTFSKLREQLPVTQEFWDNLKETEGLRQEMSKDLEEVKAK	120		
Db	61	ALGKQLNLKLLDNWDSVTSTFSKLREQLPVTQEFWDNLKETEGLRQEMSKDLEEVKAK	120		
QY	121	VQPYLDDFQKKWQEEEMELYRQKVEPLRAELQEGARQKLHELQEKLSPLGEEMRDRARHV	180		
Db	121	VQPYLDDFQKKWQEEEMELYRQKVEPLRAELQEGARQKLHELQEKLSPLGEEMRDRARHV	180		
QY	181	DALRTHLAPYSDELQRLLAARLEALKENGGARLAEYHAKATEHLSTLSEKAKPALEDLRQ	240		
Db	181	DALRTHLAPYSDELQRLLAARLEALKENGGARLAEYHAKATEHLSTLSEKAKPALEDLRQ	240		
QY	241	GLLPVLESFKVSFLSALEYTKKLNTQ	267		
Db	241	GLLPVLESFKVSFLSALEYTKKLNTQ	267		

XX The present invention describes a nucleic acid (A) encoding an  
CC apolipoprotein A-I (apoA-I) agonist (B) that is a peptide, or analog,  
CC which forms an amphipathic alpha-helix in presence of lipids. (A),  
CC optionally as a complex with lipids, and host cells that contain (A), are  
CC useful for gene therapy, or prevention, of diseases associated with  
CC dyslipidemia, specifically hypercholesterolaemia, cardiovascular disease,  
CC atherosclerosis, restenosis, HDL (high density lipoprotein) and apoA-I  
CC deficiency, hypertriglyceridemia and metabolic syndrome, also to treat  
CC endotoxemia (septic shock). Host cells containing (A) can also be used  
CC study the role of apoA-I in lipid metabolism. (B) can be used  
CC diagnostically, e.g. to measure serum HDL (particularly its subpopulation  
CC involved in retrograde cholesterol transport) and for imaging the  
CC circulatory system or HDL accumulations at fatty streaks. The present  
CC sequence represents human apoA-I

XX Sequence 267 AA;

Query Match 100.0%; Score 1362; DB 2; Length 267;  
Best Local Similarity 100.0%; Pred. No. 3.7e-99;  
Matches 267; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKA AVLTLAVLFTG SQARHFQQDEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGS 60  
Db 1 MKA AVLTLAVLFTG SQARHFQQDEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGS 60  
QY 61 ALGKQLNLKLDNWDSVTSTFSKLRQLGPGVTQEFWDNLEKETEGLRQEMSKDLEEVKAK 120  
Db 61 ALGKQLNLKLDNWDSVTSTFSKLRQLGPGVTQEFWDNLEKETEGLRQEMSKDLEEVKAK 120  
QY 121 VQPYLDDFQKKWQEMELYRQKVEPLRAELQEGARQKLHELQEKLSPLGEEMRDRARAHV 180  
Db 121 VQPYLDDFQKKWQEMELYRQKVEPLRAELQEGARQKLHELQEKLSPLGEEMRDRARAHV 180  
QY 181 DALRTHLAPYSDLRQRLAARLEALKENG GARGARLA EYHAKATEHLSTLSEKAKPALEDLRQ 240  
Db 181 DALRTHLAPYSDLRQRLAARLEALKENG GARGARLA EYHAKATEHLSTLSEKAKPALEDLRQ 240  
QY 241 GLLPVLESFKVSFLSALEEYTKKLNQ 267  
Db 241 GLLPVLESFKVSFLSALEEYTKKLNQ 267

RESULT 6  
AAB47620  
ID AAB47620 standard; protein; 267 AA.

XX AAB47620;

XX 21-JAN-2002 (first entry)

XX Full length Apo-A1.

XX Apolipoprotein; Apo-A1; Apo-A-I fragment T-cell activation inhibitor;  
KW AFT1; monocyte; IL-1; interleukin 1; TNF; tumour necrosis factor;  
KW acute pancreatitis; Alzheimer's disease; asthma; cancer; fever;  
KW inflammatory bowel disease; ischemia; multiple sclerosis; osteoporosis;  
KW Parkinson's disease; psoriasis; probe.

OS Homo sapiens.

XX Key Location/Qualifiers  
FH Peptide 25. .194  
FT /label= AFTI  
FT /note= "18 kD N-terminal fragment"  
FT 25. .144  
FT /label= AFTI  
FT /note= "13 kD N-terminal fragment"  
FT 44. .65  
FT Binding-site /label= Helical lipid binding domain  
FT 44. .65  
FT Domain /label= Amphipathic helix  
FT 66. .120

FT /label= Phylogenetically conserved domain  
FT 66. .98  
FT /label= Amphipathic helix  
FT 74. .111  
FT /note= "Involved in lipoprotein-mediated cholesterol  
FT efflux from monocytes"  
FT 90. .111  
FT /note= "Involved in lectin-cholesterol acyltransferase  
FT activity"  
FT 99. .143  
FT /label= Hinged domain  
FT 99. .120  
FT /label= Major antigenic epitope domain  
FT 99. .120  
FT /label= Amphipathic helix  
FT 121. .142  
FT /label= Amphipathic helix  
FT 143. .164  
FT /label= Amphipathic helix  
FT 149. .219  
FT /label= Receptor binding domain  
FT 156. .267  
FT /label= AFTI  
FT /note= "13 kD C-terminal fragment"  
FT 165. .208  
FT /label= Amphipathic helix  
FT 209. .219  
FT /label= Amphipathic helix  
FT 220. .241  
FT /label= Helical lipid binding domain  
FT 220. .241  
FT /label= Amphipathic helix

XX WO200168852-A2.

XX 20-SEP-2001.

XX 13-MAR-2001; 2001WO-US007826.

XX 13-MAR-2000; 2000US-0189008P.

XX (AMGE-) AMGEN INC.

PI Edwards CK, Burger D, Dayer J, Kohno T;

XX WPI; 2001-596908/67.

DR N-PSDB; AAH43623.

XX Apo-A-I fragment T-cell activation inhibitor (AFTI) polynucleotides,  
PT useful for treating, diagnosing, ameliorating diseases associated with IL  
PT -1 and/or TNF activity, e.g. acute pancreatitis, Alzheimer's disease and  
PT asthma.

XX Claim 1; Fig 1A; 132pp; English.

PS This sequence shows full length apolipoprotein (Apo-A1). Fragments of Apo  
XX -A1 may be used as Apo-A-I fragment T-cell activation inhibitors (AFTI).  
CC These fragments are selected from an 18 kD N-terminal fragment (amino  
CC acids 25-194), a 13 kD N-terminal fragment (amino acids 25-144) and a 13  
CC kD C-terminal fragment (amino acids 156-267). The AFTI polypeptides and  
CC polynucleotides are useful for regulating T-cell mediated activation of  
CC monocytes and for treating, diagnosing, ameliorating diseases associated  
CC with IL-1 and/or TNF activity. The diseases are acute pancreatitis,  
CC Alzheimer's disease, asthma, cancer, fever, inflammatory bowel disease,  
CC ischemia, multiple sclerosis, osteoporosis, Parkinson's disease or  
CC psoriasis. Numerous examples of other diseases are given in the  
CC specification. The AFTI nucleic acids are useful as hybridization probes  
CC in diagnostic assays to test for the presence of an AFTI or Apo-A-I DNA  
CC in mammalian tissue or bodily fluid samples

XX Sequence 267 AA;

SQ Query Match 100.0%; Score 1362; DB 4; Length 267;



Best Local Similarity 100.0%; Pred. No. 3.7e-99;  
Matches 267; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKA AVLTLAVLFLTGSGARHFQQDEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGS 60  
Db 1 MKA AVLTLAVLFLTGSGARHFQQDEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGS 60

QY 61 ALGKQLNLKLLDNWDSVTSTFSKLRQLGPVTQEFWDNLEKETEGRLQEMSKDLEEVKAK 120  
Db 61 ALGKQLNLKLLDNWDSVTSTFSKLRQLGPVTQEFWDNLEKETEGRLQEMSKDLEEVKAK 120

QY 121 VQPYLDDFQKKWQEEEMELYRQKVEPLRAELQEGARQKLHELQEKLSPLGEEMDRARAHV 180  
Db 121 VQPYLDDFQKKWQEEEMELYRQKVEPLRAELQEGARQKLHELQEKLSPLGEEMDRARAHV 180

QY 181 DALRTHLAPYSDELRLQRLAARLEALKENG GARLA EYHAKATEHLSTLSEKAKPALEDLRQ 240  
Db 181 DALRTHLAPYSDELRLQRLAARLEALKENG GARLA EYHAKATEHLSTLSEKAKPALEDLRQ 240

QY 241 GLLPVLESFKVSFLSAL E EYTKKLNTQ 267  
Db 241 GLLPVLESFKVSFLSAL E EYTKKLNTQ 267

RESULT 7  
AAO15892

ID AAO15892 standard; protein; 267 AA.

XX

AC AAO15892;

XX

DT 30-JAN-2003 (first entry)

XX

DE Human apolipoprotein A-1 (APOA1).

XX

KW Human; gene therapy; single nucleotide polymorphism; SNP;

KW cytochrome C oxidase subunit V1b; COX6B; high serum cholesterol; GPI-1;

KW N-acetylglucosaminyl transferase component; cardiovascular disease; HDL;

KW glycosylphosphatidylinositol-1; low serum high density lipoprotein.

XX

OS Homo sapiens.

XX

PN WO200272604-A2.

XX

PD 19-SEP-2002.

XX

PF 05-MAR-2002; 2002WO-US0006728.

XX

PR 09-MAR-2001; 2001US-00802640.

XX

PA (SEQU-) SEQUENOM INC.

XX

PI Braun A, Bansal A, Kley n PW;

XX

DR WPI; 2002-750478/81.

XX

DR N-PSDB; ABT13014.

XX

PT Detecting the presence or absence of an allelic variant of a polymorphic

PT region of COX6B and/or GPI-1 gene, useful for detecting a predisposition

PT to high serum cholesterol, low serum HDL and cardiovascular disease.

XX

PS Disclosure; Page 137-138; 199pp; English.

XX

CC The invention comprises methods of detecting the presence or absence of

CC at least one allelic variant of a polymorphic region of a gene associated

CC with cardiovascular disease. The invention specifically relates to

CC detecting the region of a cytochrome C oxidase subunit V1b (COX6B) gene

CC that is associated with high serum cholesterol, or the region of the N-

CC acetylglucosaminyl transferase component glycosylphosphatidylinositol-1

CC (GPI-1) gene that is associated with low serum high density lipoprotein

CC (HDL). The methods of the invention are useful for detecting a

CC predisposition to high serum cholesterol, low serum HDL and

CC cardiovascular disease. The methods are also useful for elucidating

CC pathological pathways, developing diagnostic assays and new drug

CC therapies for such disorders. The present amino acid sequence represents

CC a human protein that is associated with high serum cholesterol, low serum

CC HDL and/or cardiovascular disease

XX

SQ Sequence 267 AA;

Query Match 100.0%; Score 1362; DB 5; Length 267;

Best Local Similarity 100.0%; Pred. No. 3.7e-99;

Matches 267; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKA AVLTLAVLFLTGSGARHFQQDEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGS 60

Db 1 MKA AVLTLAVLFLTGSGARHFQQDEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGS 60

QY 61 ALGKQLNLKLLDNWDSVTSTFSKLRQLGPVTQEFWDNLEKETEGRLQEMSKDLEEVKAK 120

Db 61 ALGKQLNLKLLDNWDSVTSTFSKLRQLGPVTQEFWDNLEKETEGRLQEMSKDLEEVKAK 120

QY 121 VQPYLDDFQKKWQEEEMELYRQKVEPLRAELQEGARQKLHELQEKLSPLGEEMDRARAHV 180

Db 121 VQPYLDDFQKKWQEEEMELYRQKVEPLRAELQEGARQKLHELQEKLSPLGEEMDRARAHV 180

QY 181 DALRTHLAPYSDELRLQRLAARLEALKENG GARLA EYHAKATEHLSTLSEKAKPALEDLRQ 240

Db 181 DALRTHLAPYSDELRLQRLAARLEALKENG GARLA EYHAKATEHLSTLSEKAKPALEDLRQ 240

QY 241 GLLPVLESFKVSFLSAL E EYTKKLNTQ 267

Db 241 GLLPVLESFKVSFLSAL E EYTKKLNTQ 267

RESULT 8  
ABG97593

ID ABG97593 standard; protein; 267 AA.

XX

AC ABG97593;

XX

DT 17-DEC-2002 (first entry)

XX

DE Human apolipoprotein analogue 1 (Apo A1) protein #15.

XX

KW Apolipoprotein analogue; Apo A; arteriosclerosis; endotoxin removal;

KW angina pectoris; myocardial infarction; arterial stenosis; claudication;

KW carotis stenosis; cerebral arterial stenosis; gene therapy; cholesterol;

KW cardiovascular disease.

XX

OS Homo sapiens.

XX

PN WO200238609-A2.

XX

PD 16-MAY-2002.

XX

PF 09-NOV-2001; 2001WO-DK0000739.

XX

PR 10-NOV-2000; 2000DK-00001682.

XX

PR 15-JAN-2001; 2001DK-00000057.

XX

PR 26-JAN-2001; 2001US-0264022P.

XX

PA (PROT-) PROTEOPHARMA APS.

XX

PI Graversen J, Moestrup S;

XX

DR WPI; 2002-527481/56.

XX

PT Novel apolipoprotein construct comprising apolipoprotein A linked to

PT carbohydrate, peptide or protein heterologous group, useful for treating

PT plaque/unstable angina pectoris, myocardial infarction, arterial

PT stenoses.

XX

PS Disclosure; Fig 1; 113pp; English.

XX The invention describes an Apolipoprotein (Apo) construct (I) for use as

CC medicament having general formula apo-A-X, where apo-A is an

CC apolipoprotein component such as apolipoprotein AI, AII or AIV, or its  
CC analogue or variant, and X is heterologous group e.g., amino acid,  
CC peptide, protein, carbohydrate or a nucleic acid, providing that when (I)  
CC consists of exactly two identical, native apolipoproteins these are  
CC linked serially. (I) is useful for preparing a pharmaceutical composition  
CC which further comprises excipients, adjuvants, additives, such as  
CC phospholipids, cholesterol or triglycerides. (I) is useful or treating  
CC and/or preventing arteriosclerosis, for removing endotoxins, for treating  
CC angina pectoris including plaque or unstable angina pectoris, myocardial  
CC infarction, arterial stenoses such as claudicatio, carotis stenosis,  
CC cerebral arterial stenosis and other cardiovascular diseases. The nucleic  
CC acid (II) encoding (I) is useful for gene therapy, where the DNA sequence  
CC encoding (I) is used for transfection or infection of at least one cell  
CC population comprising macrophages or liver cells. (I) has a half-life of  
CC at least the half-life of native apoA-I, A-II or A-IV, preferably two  
CC times higher or more preferably 10 times higher than the half-life of the  
CC apoA molecules. (I) also has a higher binding affinity to cholesterol  
CC compared to native apoA-I, A-II or A-IV. (I) causes substantially no  
CC immune response in humans. This is the amino acid sequence of a human  
CC apolipoprotein (Apo) analogue fragment

XX Sequence 267 AA;

Query Match 100.0%; Score 1362; DB 5; Length 267;  
Best Local Similarity 100.0%; Pred. No. 3.7e-99;  
Matches 267; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 MKAAVLTTLAVLFLTGSGQARHFQQDEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGS 60  
Db 1 MKAAVLTTLAVLFLTGSGQARHFQQDEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGS 60  
  
QY 61 ALGKQLNLKLLDNWDSVTSTFSKLRQLGPTQEFWDNLEKETEGLRQEMSKDLEEVKAK 120  
Db 61 ALGKQLNLKLLDNWDSVTSTFSKLRQLGPTQEFWDNLEKETEGLRQEMSKDLEEVKAK 120  
  
QY 121 VQPYLDDFQKKWQEEEMELYRQKVEPLRAELQEGARQKLHELQEKLSPLGHEMRDRARAHV 180  
Db 121 VQPYLDDFQKKWQEEEMELYRQKVEPLRAELQEGARQKLHELQEKLSPLGHEMRDRARAHV 180  
  
QY 181 DALRTHLAPYSDELQRLAARLEALKENGCGARLAEYHAKATEHLSTLSEKAKPALEDLRQ 240  
Db 181 DALRTHLAPYSDELQRLAARLEALKENGCGARLAEYHAKATEHLSTLSEKAKPALEDLRQ 240  
  
QY 241 GLLPVLESFKVSFLSALAEYTKKLNNTQ 267  
Db 241 GLLPVLESFKVSFLSALAEYTKKLNNTQ 267

RESULT 9  
ABR44031  
ID ABR44031 standard; protein; 267 AA.  
XX ABR44031;  
AC ABR44031;  
XX 04-AUG-2003 (first entry)  
XX Human apolipoprotein A-I (ApoA-I) protein.  
DE Human apolipoprotein A-I (ApoA-I) protein.  
XX Apolipoprotein A-I; ApoA-I; cardiant; gene therapy; human;  
KW Apolipoprotein A-I; ApoA-I; cardiant; gene therapy; human;  
KW cardiovascular disorder.  
XX Homo sapiens.  
OS Homo sapiens.  
XX Key Location/Qualifiers  
FH Misc-difference 178 /label= L178P  
FT /note= "wild-type Leu can be replaced with Pro"  
FT /note= "wild-type Leu can be replaced with Pro"  
XX WO2003035691-A1.  
PN WO2003035691-A1.  
XX 01-MAY-2003.  
PD 01-MAY-2003.  
XX 25-OCT-2002; 2002WO-CA001615.

XX 26-OCT-2001; 2001US-0335075P.  
PR (XENO-) XENON GENETICS INC.  
XX (XENO-) XENON GENETICS INC.  
PA (UYBR-) UNIV BRITISH COLUMBIA.  
XX Brownlie AJ, Dube M, Samuels M, Hayden MR;  
PI WPI; 2003-449258/42.  
XX N-PSDB; ACC48172.  
XX New Apolipoprotein A-1 mutation, useful for preparing a composition for  
PT treating cardiovascular disorder.  
XX Claim 19; Page 33; 52pp; English.  
XX The invention relates to a mutation of the apolipoprotein A-I (ApoA-I)  
CC comprising a leucine to proline variant in position 178. The mutant ApoA-  
CC I polynucleotide is useful for preparing a composition for treating  
CC cardiovascular disorder. The present sequence represents a human ApoA-I  
CC wild-type protein  
XX Sequence 267 AA;  
SQ Query Match 100.0%; Score 1362; DB 6; Length 267;  
Best Local Similarity 100.0%; Pred. No. 3.7e-99;  
Matches 267; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 MKAAVLTTLAVLFLTGSGQARHFQQDEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGS 60  
Db 1 MKAAVLTTLAVLFLTGSGQARHFQQDEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGS 60  
  
QY 61 ALGKQLNLKLLDNWDSVTSTFSKLRQLGPTQEFWDNLEKETEGLRQEMSKDLEEVKAK 120  
Db 61 ALGKQLNLKLLDNWDSVTSTFSKLRQLGPTQEFWDNLEKETEGLRQEMSKDLEEVKAK 120  
  
QY 121 VQPYLDDFQKKWQEEEMELYRQKVEPLRAELQEGARQKLHELQEKLSPLGHEMRDRARAHV 180  
Db 121 VQPYLDDFQKKWQEEEMELYRQKVEPLRAELQEGARQKLHELQEKLSPLGHEMRDRARAHV 180  
  
QY 181 DALRTHLAPYSDELQRLAARLEALKENGCGARLAEYHAKATEHLSTLSEKAKPALEDLRQ 240  
Db 181 DALRTHLAPYSDELQRLAARLEALKENGCGARLAEYHAKATEHLSTLSEKAKPALEDLRQ 240  
  
QY 241 GLLPVLESFKVSFLSALAEYTKKLNNTQ 267  
Db 241 GLLPVLESFKVSFLSALAEYTKKLNNTQ 267

RESULT 10  
ABP57065  
ID ABP57065 standard; protein; 267 AA.  
XX ABP57065;  
AC ABP57065;  
XX 14-APR-2003 (first entry)  
DT 14-APR-2003 (first entry)  
XX Human apolipoprotein (APOA1) protein SEQ ID NO:10.  
DE Human apolipoprotein (APOA1) protein SEQ ID NO:10.  
XX Atherosclerosis; pro-atherogenic inhibitor; antiatherosclerotic;  
KW macrophage-specific expression element; gene therapy; apolipoprotein;  
KW APOA1.  
XX Homo sapiens.  
OS Homo sapiens.  
XX WO2003002061-A2.  
PN WO2003002061-A2.  
XX 09-JAN-2003.  
PD 09-JAN-2003.  
XX 26-JUN-2002; 2002WO-US020350.  
PF 26-JUN-2002; 2002WO-US020350.  
XX 26-JUN-2001; 2001US-00893366.  
XX

PA (UYSA-) UNIV SAN DIEGO STATE FOUND.  
XX Davis RA;  
PI WPI; 2003-201457/19.  
XX N-PSDB; ABZ59334.  
DR Novel nucleic acid useful for inhibiting or reducing atherosclerosis,  
XX comprises nucleotide sequence encoding an inhibitor of a pro-atherogenic  
PT molecule operationally linked to a macrophage-specific expression  
PT element.  
XX  
PS Disclosure; Page 95; 99pp; English.  
XX  
CC The present invention describes a nucleic acid (I) comprising a  
CC nucleotide sequence encoding an inhibitor of a pro-atherogenic molecule  
CC operationally linked to a macrophage-specific expression element. Also  
CC described: (1) a vector (II) comprising (I); (2) an embryonic stem cell  
CC (III) comprising (I); (3) an isolated mammalian cell (IV) comprising (I);  
CC (4) a recombinant cell (V) comprising a macrophage expressing nucleic  
CC acid encoding an inhibitor of a pro-atherogenic molecule; (5) a  
CC transgenic non-human mammal (VI) comprising recombinant cells containing  
CC a transgenic nucleic acid encoding an inhibitor of a pro-atherogenic  
CC molecule; and (6) a non-human mammalian cell (VII) isolated from (VI).  
CC (I) has antiatherosclerotic activity and can be used in gene therapy. (I)  
CC or (V) can be used for inhibiting or reducing atherosclerosis, by  
CC administering to an individual (I) or a population of (V), where the  
CC population of (V) is derived from leukocytes, monocytes, macrophages or  
CC stem cells. (V) or (VI) is useful to screen for a drug potentially  
CC effective for treating atherosclerosis. (V) is useful for identifying a  
CC compound that reduces susceptibility to developing atherosclerosis. (VI)  
CC is useful for determining the role of an inhibitor of pro-atherogenic  
CC molecule in a particular pathological phenotype or condition of an animal  
CC model for atherosclerosis used in drug development. The present sequence  
CC represents human apolipoprotein (APOA1), which is given in the  
CC exemplification of the present invention  
XX  
SQ Sequence 267 AA;

Query Match 100.0%; Score 1362; DB 6; Length 267;  
Best Local Similarity 100.0%; Pred. No. 3.7e-99;  
Matches 267; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKA AVLTLAVFLTGSQARHFQQDEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGS 60  
Db |||||  
QY 1 MKA AVLTLAVFLTGSQARHFQQDEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGS 60  
Db |||||  
QY 61 ALGKQLNLKLLDNWDSVTSTFSKLRQLGPVTQEFWDNLEKETEGLRQEMSKDLEEVKAK 120  
Db |||||  
QY 61 ALGKQLNLKLLDNWDSVTSTFSKLRQLGPVTQEFWDNLEKETEGLRQEMSKDLEEVKAK 120  
Db |||||  
QY 121 VQPYLDDFQKKWQEEEMELYRQKVEPLRAELQEGARQKLHELQEKLSPLGEEMRDRARAHV 180  
Db |||||  
QY 121 VQPYLDDFQKKWQEEEMELYRQKVEPLRAELQEGARQKLHELQEKLSPLGEEMRDRARAHV 180  
Db |||||  
QY 181 DALRTHLAPYSDELRLQRLAARLEALKENGGLARLAHYHAKATEHLSTLSEKAKPALEDLRQ 240  
Db |||||  
QY 181 DALRTHLAPYSDELRLQRLAARLEALKENGGLARLAHYHAKATEHLSTLSEKAKPALEDLRQ 240  
Db |||||  
QY 241 GLLPVLESFKVSFLSALEYTKKLNQ 267  
Db |||||  
QY 241 GLLPVLESFKVSFLSALEYTKKLNQ 267  
Db |||||

RESULT 11  
ADA61214  
ID ADA61214 standard; protein; 267 AA.  
XX  
AC ADA61214;  
XX  
DT 20-NOV-2003 (first entry)  
XX  
DE Human apolipoprotein A-1 (apo-A-1).

XX Human; apolipoprotein A-I; apo-A-I; T-cell activation inhibitor-like;  
KW AFTI; T-cell-mediated activation; monocyte; interleukin-lbета; IL-lbета;  
KW tumour necrosis factor alpha; TNF-alpha; gene therapy;  
KW IL-l-mediated disease; acute pancreatitis; Alzheimer's disease; asthma;  
KW cancer; diabetes; glomerulonephritis; multiple sclerosis; osteoporosis;  
KW pain; Parkinson's disease; psoriasis; uveitis; TNF-mediated disease;  
KW depression; pancreatitis; periodontal disease; pulmonary fibrosis;  
KW reperfusion injury; rheumatic disease; septic shock;  
KW systemic lupus erythematosus; thyroiditis; neurotropic; neuroprotective;  
KW cytostatic; nephrotropic; analgesic; ophthalmological; antiinflammatory;  
KW vasotropic; antibacterial; immunosuppressive; dermatological.  
XX  
OS Homo sapiens.  
XX  
PN US2002064820-A1.  
XX  
PD 30-MAY-2002.  
XX  
PF 13-MAR-2001; 2001US-00803918.  
XX  
PR 13-MAR-2000; 2000US-0189008P.  
PR 31-MAR-2000; 2000US-0193551P.  
XX  
PA (DAYE/) DAYER J.  
PA (BURG/) BURGER D.  
PA (KOHN/) KOHNO T.  
PA (EDWA/) EDWARDS C K.  
XX  
PI Dayer J, Burger D, Kohno T, Edwards CK;  
XX WPI; 2003-615701/58.  
XX N-PSDB; ADA61213.  
XX  
PT New apolipoprotein A-I polypeptide or its related polypeptide termed apo-  
PT A-I fragment T-cell activation inhibitor-like polypeptide, useful for  
PT treating interleukin-1 or tumor necrosis factor-alpha mediated disease.  
XX  
PS Claim 1; Fig 1A; 56pp; English.  
XX  
CC The invention discloses a apolipoprotein A-I (apo-A-I) polypeptide or its  
CC related polypeptide, apo-A-I fragment T-cell activation inhibitor-like  
CC (AFTI) polypeptide, or a fragment or an allelic or splice variant. Apo-A-  
CC I and its derivatives are used in regulating T-cell-mediated activation  
CC of monocytes. Also disclosed is an antibody produced by immunising an  
CC animal with apo-A-I and a selective binding agent, or its fragment. Apo-A  
CC -I is useful for reducing inflammation, interleukin (IL)-lbета secretion  
CC or tumour necrosis factor (TNF)-alpha secretion in a subject, or for  
CC treating IL-1 or TNF-alpha mediated disease in a subject. The  
CC compositions of the invention are useful for treating (e.g. gene  
CC therapy), preventing or ameliorating a medical condition involving  
CC monocyte activation in a patient, for determining whether a compound  
CC inhibits activity or production of apo-A-I, for detecting or quantifying  
CC the amount of apo-A-I in a sample, for regulating T-cell-mediated  
CC activation of monocytes, to identify a molecule that binds to apo-A-I,  
CC for identifying AFTI receptors, for cloning AFTI receptors, and as an  
CC immunogen to raise antibodies, for treating acute and chronic IL-1-  
CC mediated diseases such as acute pancreatitis, Alzheimer's disease,  
CC asthma, cancer, diabetes, glomerulonephritis, multiple sclerosis,  
CC osteoporosis, pain, Parkinson's disease, psoriasis, uveitis, and acute  
CC and chronic TNF-mediated diseases such as depression, pancreatitis,  
CC periodontal diseases, pulmonary fibrosis, reperfusion injury, rheumatic  
CC diseases, septic shock, systemic lupus erythematosus and thyroiditis.  
CC They are also useful for regulating expression and modulating levels of  
CC apo-A-I, as hybridisation probes in diagnostic assays, for diagnostic  
CC applications, to test for the presence of apo-A-I in cells, for in vivo  
CC imaging and in therapeutics. The sequence presented is the human apo-A-1  
CC protein which comprises an 18K N-terminal or 13K N- or C-terminal  
CC fragments of the apo-A-1 protein.  
XX  
SQ Sequence 267 AA;

Query Match 100.0%; Score 1362; DB 6; Length 267;

		Best Local Similarity 100.0%; Pred. No. 3.7e-99;		Matches 267; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1	MKAAVLT LAVLFLTGSQARHFQQDEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGS	60		
Db	1	MKAAVLT LAVLFLTGSQARHFQQDEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGS	60		
QY	61	ALGKQLNLKLLDNWDSVTSTFSKLRQLGPGVTQEFWDNLEKETEGRLQEMSKDLEEVKAK	120		
Db	61	ALGKQLNLKLLDNWDSVTSTFSKLRQLGPGVTQEFWDNLEKETEGRLQEMSKDLEEVKAK	120		
QY	121	VQPYLDDFQKKWQEEEMELYRQKVEPLRAELQEGARQKLHELQEKLSPLGEEMRDRARAHV	180		
Db	121	VQPYLDDFQKKWQEEEMELYRQKVEPLRAELQEGARQKLHELQEKLSPLGEEMRDRARAHV	180		
QY	181	DALRTHLAPYSDELQRQLAARLEALKENGGARLAEYHAKATEHLSLSEKAKPALEDLRQ	240		
Db	181	DALRTHLAPYSDELQRQLAARLEALKENGGARLAEYHAKATEHLSLSEKAKPALEDLRQ	240		
QY	241	GLLPVLESFKVSFLSALEEYTKKLNQ	267		
Db	241	GLLPVLESFKVSFLSALEEYTKKLNQ	267		
RESULT 12					
ADJ83084					
ID	ADJ83084 standard; protein; 267 AA.				
XX					
AC	ADJ83084;				
XX					
DT	06-MAY-2004 (first entry)				
XX					
DE	Human apolipoprotein A-I precursor protein - SEQ ID 75.				
XX					
KW	NOVX; cytostatic; antiarteriosclerotic; antidiabetic; antiasthmatic; antiallergic; antiinflammatory; respiratory; antiarthritic; dermatological; antibacterial; cerebroprotective; vasotropic; cardiant; haemostatic; hypotensive; hepatotropic; neuroprotective; anorectic; nootropic; antiulcer; muscular; immunosuppressive; gynaecological; antiopioratic; endocrine; ophthalmological; osteopathic; antiparkinsonian; anticonvulsant; tranquiliser; analgesic; nephrotropic; antiinfertility; antilipaemic; cardiomyopathy; atherosclerosis; diabetes; cell signal processing; metabolic pathway; asthma; allergy; emphysema; autoimmune; graft-versus-host; arthritis; cancer; stroke; haemophilia; obesity; Alzheimer's; pain; chromosome mapping; tissue typing; human; apolipoprotein A-I precursor.				
XX					
OS	Homo sapiens.				
XX					
PN	US2003170630-A1.				
XX					
PD	11-SEP-2003.				
XX					
PF	21-DEC-2001; 2001US-00032189.				
XX					
PR	21-DEC-2000; 2000US-0257495P.				
PR	22-DEC-2000; 2000US-0258171P.				
PR	20-FEB-2001; 2001US-0269940P.				
PR	08-MAR-2001; 2001US-0274192P.				
PR	22-MAR-2001; 2001US-0277826P.				
PR	29-MAR-2001; 2001US-0279840P.				
PR	11-APR-2001; 2001US-0282981P.				
PR	13-APR-2001; 2001US-0283656P.				
PR	31-JUL-2001; 2001US-0309247P.				
PR	10-AUG-2001; 2001US-0311754P.				
PR	17-AUG-2001; 2001US-0313331P.				
XX					
PA	(ALSO/) ALSOBROOK J P.				
PA	(TCHE/) TCHERNEV V T.				
PA	(LIUX/) LIU X.				
PA	(SPYT/) SPYTEK K A.				
PA	(ZERH/) ZERHUSEN B D.				
PA	(PATT/) PATTURAJAN M.				
		Best Local Similarity 100.0%; Pred. No. 3.7e-99;		Matches 267; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
PA	(LEPL/)	LEPLEY D M.			
PA	(BURG/)	BURGESS C E.			
PA	(SHIM/)	SHIMKETS R A.			
PA	(GROS/)	GROSSE W M.			
PA	(SEK/)	SZEKERES E S.			
PA	(VERN/)	VERNET C A M.			
PA	(LILL/)	LI L.			
PA	(CASM/)	CASMAN S J.			
PA	(BOLD/)	BOLDOG F L.			
PA	(GORM/)	GORMAN L.			
PA	(GANG/)	GANGOLLI E A.			
PA	(FERN/)	FERNANDES E R.			
PA	(RIEG/)	RIEGER D K.			
PA	(EDIN/)	EDINGER S R.			
PA	(GUNT/)	GUNTHER E.			
PA	(MILL/)	MILLET I.			
PA	(SCIO/)	SCIORE P.			
PA	(ELLE/)	ELLERMAN K.			
PA	(MACD/)	MACDOUGALL J R.			
PA	(SMIT/)	SMITHSON G.			
XX					
PI	Alsobrook JP, Tchernev VT, Liu X, Spytek KA, Zerhusen BD; Patturajan M, Lepley DM, Burgess CE, Shimkets RA, Grosse WM; Szekeres ES, Vernet CAM, Li L, Casman SJ, Boldog FL, Gorman L; Gangolli EA, Fernandes ER, Rieger DK, Edinger SR, Gunther E; Millet I, Sciore P, Ellerman K, Macdougall JR, Smithson G; WPI; 2003-898249/82.				
DR					
XX					
PT	New NOVX polypeptides and nucleic acid molecules, useful for diagnosing, preventing or treating NOVX-associated polypeptide disorder, e.g. cardiomyopathy, atherosclerosis, diabetes, cancer, parkinson's disease or asthma.				
PT					
PT					
XX					
PS	Disclosure; SEQ ID NO 75; 263pp; English.				
XX					
CC	The invention relates to a novel isolated NOVX polypeptide. The polypeptide demonstrates cytostatic, antiarteriosclerotic, antidiabetic, antiasthmatic, antiallergic, antiinflammatory, respiratory, antiarthritic, dermatological, antibacterial, cerebroprotective, antiasthmatic, cardiant, haemostatic, hypotensive, hepatotropic, neuroprotective, anorectic, nootropic, antiulcer, muscular, immunosuppressive, gynaecological, antiparkinsonian, anticonvulsant, ophthalmological, osteopathic, antiparkinsonian, antiinfertility and antilipaemic tranquiliser, analgesic, nephrotropic, antiinfertility and antilipaemic activities. The NOVX polypeptide, nucleic acid or antibody of the invention may be useful for treating or preventing a NOVX-associated disorder, such as cardiomyopathy, atherosclerosis, diabetes or a disorder related to cell signal processing and metabolic pathway modulation. Furthermore, the NOVX polypeptides may be useful for diagnosing, treating or preventing diseases such as asthma, allergies, emphysema, autoimmune disease, graft-versus-host disease, arthritis, cancer, stroke, haemophilia, obesity, Alzheimer's disease and pain. The nucleic acids may be used as hybridisation probes, in chromosome mapping, tissue typing, preventive medicine or pharmacogenomics. The current sequence is that of a protein of the invention which is related to human NOVX protein.				
XX	Sequence 267 AA;				
SQ					
		Query Match 100.0%; Score 1362; DB 7; Length 267;			
		Best Local Similarity 100.0%; Pred. No. 3.7e-99;			
		Matches 267; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
QY	1	MKAAVLT LAVLFLTGSQARHFQQDEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGS	60		
Db	1	MKAAVLT LAVLFLTGSQARHFQQDEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGS	60		
QY	61	ALGKQLNLKLLDNWDSVTSTFSKLRQLGPGVTQEFWDNLEKETEGRLQEMSKDLEEVKAK	120		
Db	61	ALGKQLNLKLLDNWDSVTSTFSKLRQLGPGVTQEFWDNLEKETEGRLQEMSKDLEEVKAK	120		
QY	121	VQPYLDDFQKKWQEEEMELYRQKVEPLRAELQEGARQKLHELQEKLSPLGEEMRDRARAHV	180		



Db 121 VQPYLDDFQKKWQEMELYRQKVEPLRAELQEGARQKHLHLEQKLSPLGEMRDRARAHV 180

QY 181 DALRTHLAPYSDELRLQRLAARLEALKENGARLAAYHAKATEHLSTLSEKAKPALEDLRQ 240

Db 181 DALRTHLAPYSDELRLQRLAARLEALKENGARLAAYHAKATEHLSTLSEKAKPALEDLRQ 240

QY 241 GLLPVLESFKVSFLSALEEYTKKLNTQ 267

Db 241 GLLPVLESFKVSFLSALEEYTKKLNTQ 267

RESULT 13

ADI19752

ID ADI19752 standard; protein; 267 AA.

XX

AC ADI19752;

XX

DT 22-APR-2004 (first entry)

XX

DE Human APOA1 protein.

XX

KW Pro-atherogenic; atherosclerosis; therapy; human; apolipoprotein; APOA1;

KW macrophage-specific expression element.

XX

OS Homo sapiens.

XX

PN US2004001810-A1.

XX

PD 01-JAN-2004.

XX

PF 26-JUN-2002; 2002US-00186288.

XX

PR 26-JUN-2002; 2002US-00186288.

XX

PA (DAVI/) DAVIS R A.

XX

PI Davis RA;

XX

DR WPI; 2004-061641/06.

DR N-PSDB; ADI19751.

DR GENBANK; XM\_006435.

XX

PT New nucleic acids encoding an inhibitor of a pro-atherogenic molecule

PT operationally linked to a macrophage-specific expression element, useful

PT for reducing or inhibiting atherosclerosis.

XX

PS Disclosure; SEQ ID NO 10; 45pp; English.

XX

CC The present invention provides a nucleic acid comprising a nucleotide

CC sequence encoding an inhibitor of a pro-atherogenic molecule

CC operationally linked to a macrophage-specific expression element. The

CC invention is useful for reducing and inhibiting atherosclerosis. The

CC present sequence is human apolipoprotein (APOA1) protein.

XX

SQ Sequence 267 AA;

Query Match 100.0%; Score 1362; DB 8; Length 267;

Best Local Similarity 100.0%; Pred. No. 3.7e-99;

Matches 267; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKAAVLTAVLFLTGSAQHFQQDEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGS 60

Db 1 MKAAVLTAVLFLTGSAQHFQQDEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGS 60

QY 61 ALGKQLNLKLLDNWDSVTSTFSKRLQGLGPVTQEFWDNLEKETEGRLQEMSKDLEEVKAK 120

Db 61 ALGKQLNLKLLDNWDSVTSTFSKRLQGLGPVTQEFWDNLEKETEGRLQEMSKDLEEVKAK 120

QY 121 VQPYLDDFQKKWQEMELYRQKVEPLRAELQEGARQKHLHLEQKLSPLGEMRDRARAHV 180

Db 121 VQPYLDDFQKKWQEMELYRQKVEPLRAELQEGARQKHLHLEQKLSPLGEMRDRARAHV 180

QY 181 DALRTHLAPYSDELRLQRLAARLEALKENGARLAAYHAKATEHLSTLSEKAKPALEDLRQ 240

Db 181 DALRTHLAPYSDELRLQRLAARLEALKENGARLAAYHAKATEHLSTLSEKAKPALEDLRQ 240

QY 241 GLLPVLESFKVSFLSALEEYTKKLNTQ 267

Db 241 GLLPVLESFKVSFLSALEEYTKKLNTQ 267

RESULT 14

ABM81308

ID ABM81308 standard; protein; 267 AA.

XX

AC ABM81308;

XX

DT 18-NOV-2004 (first entry)

XX

DE Tumour-associated antigenic target (TAT) polypeptide PRO36215, SEQ:3377.

XX

KW Tumour-associated antigenic target; TAT; human; overexpression; cancer;

KW tumour; diagnosis; cell proliferative disorder; breast cancer;

KW colorectal cancer; lung cancer; ovarian cancer; liver cancer;

KW central nervous system cancer; bladder cancer; pancreatic cancer;

KW cervical cancer; melanoma; leukaemia; hybridisation probe;

KW chromosome identification; chromosome mapping; gene mapping;

XX

OS Homo sapiens.

XX

PN WO2004030615-A2.

XX

PD 15-APR-2004.

XX

PF 29-SEP-2003; 2003WO-US028547.

XX

PR 02-OCT-2002; 2002US-0414971P.

XX

PA (GETH ) GENENTECH INC.

XX

PI Wu TD, Zhang Z, Zhou Y;

XX

DR WPI; 2004-347921/32.

DR N-PSDB; ACN39312.

XX

PT New tumor-associated antigenic target polypeptides and nucleic acids,

PT useful in preparing a medicament for treating or detecting a

PT proliferative disorder, e.g. breast, lung, colorectal, ovarian or

PT prostate cancer or tumor.

XX

PS Claim 12; SEQ ID NO 3377; 7273pp; English.

XX

CC The invention relates to human tumour-associated antigenic target (TAT)

CC polypeptides, and their related nucleic acids. The TAT polypeptides are

CC overexpressed in cancer tissues compared to normal tissues, and may thus

CC serve as effective targets for the diagnosis and treatment of cancer in

CC mammals. The invention also relates to nucleic acid and polypeptide

CC sequences at least 80% identical to the TAT nucleic acids and

CC polypeptides; expression vectors and host cells comprising a TAT nucleic

CC acid; an antibody specific for a TAT polypeptide; a peptide or organic

CC molecule which binds to a TAT polypeptide; fusion proteins comprising a

CC TAT polypeptide; and methods and compositions for the treatment or

CC diagnosis of cancer in mammals. TAT polypeptides, nucleic acids,

CC antibodies, antagonists, binding molecules and compositions are useful

CC for diagnosing or treating a cell proliferative disorder associated with

CC increased TAT expression, particularly cancers such as breast cancer,

CC colorectal cancer, lung cancer, ovarian cancer, liver cancer, bladder

CC cancer, pancreatic cancer, cervical cancer, cancers of the central

CC nervous system, melanoma and leukaemia. TAT nucleic acids may further be

CC used as hybridisation probes, in chromosome and gene mapping, in

CC chromosome identification and in gene therapy. The present sequence

XX represents a TAT polypeptide of the invention

SQ Sequence 267 AA;



GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 28, 2006, 20:23:53 ; Search time 41 Seconds  
(without alignments)  
626.582 Million cell updates/sec

Title: US-09-803-918A-2  
Perfect score: 1362  
Sequence: 1 MKAAVLTLAVLFLTGSQARH.....SFKVSFLSALIEYTKQLNTQ 267

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 80:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1362	100.0	267	1	LPHUA1	apolipoprotein A-I
2	1306	95.9	267	2	JS0079	apolipoprotein A-I
3	1299	95.4	267	1	A26529	apolipoprotein A-I
4	1161.5	85.3	266	1	LPDGA1	apolipoprotein A-I
5	1100.5	80.8	266	1	LPRB1Z	apolipoprotein A-I
6	1100	80.8	265	2	A46018	apolipoprotein AI
7	1093	80.2	265	2	JT0672	apolipoprotein A-I
8	1087.5	79.8	264	2	S31394	apolipoprotein A-I
9	1082	79.4	265	1	LPRB1B	apolipoprotein A-I
10	1082	79.4	265	2	A56858	apolipoprotein A-I
11	974.5	71.5	241	2	A24998	apolipoprotein A-I
12	924	67.8	231	2	JQ0704	apolipoprotein A-I
13	904.5	66.4	264	2	S22420	apolipoprotein A-I
14	898.5	66.0	262	2	JC1237	apolipoprotein A-I
15	849.5	62.4	259	2	A24700	apolipoprotein A-I
16	688.5	50.6	264	1	LPCHA1	apolipoprotein A-I
17	663.5	48.7	264	2	JC5456	apolipoprotein A-I
18	644.5	47.3	246	2	A61448	apolipoprotein A-I
19	617.5	45.3	164	2	S21830	apolipoprotein A-I
20	291	21.4	429	2	S29565	apolipoprotein A-I
21	278.5	20.4	396	1	LPHUA4	apolipoprotein A-I
22	267	19.6	391	1	LPRTA4	apolipoprotein A-I
23	253	18.6	399	2	C40892	apolipoprotein A-I
24	251	18.4	391	2	B40892	apolipoprotein A-I
25	251	18.4	395	2	A40892	apolipoprotein A-I
26	249.5	18.3	401	2	A47141	apolipoprotein A-I
27	238.5	17.5	394	2	A25281	apolipoprotein A-I
28	225.5	16.6	258	2	JH0472	apolipoprotein A-I
29	209	15.3	311	2	JU0036	apolipoprotein E p

30	198	14.5	312	1	LPRTE	apolipoprotein E p
31	194.5	14.3	1547	2	T28657	blackjack protein,
32	190.5	14.0	317	2	A28792	apolipoprotein E p
33	189.5	13.9	317	2	S03185	apolipoprotein E p
34	188	13.8	317	2	S33450	apolipoprotein E -
35	184	13.5	298	2	S12635	apolipoprotein E p
36	182	13.4	329	2	JC5566	apolipoprotein E p
37	178.5	13.1	291	2	C60940	apolipoprotein E -
38	174.5	12.8	317	1	LPHUB	apolipoprotein E p
39	166.5	12.2	316	2	JC6549	apolipoprotein E p
40	160	11.7	316	2	I45996	apolipoprotein E -
41	160	11.7	316	2	S26478	apolipoprotein E -
42	147	10.8	311	2	A45951	apolipoprotein E p
43	146	10.7	513	2	S08381	keratin, 58K type
44	143.5	10.5	771	1	A33430	h-caldesmon - Chic
45	137	10.1	470	2	T23512	hypothetical prote

ALIGNMENTS

RESULT 1  
LPHUA1

apolipoprotein A-I precursor [validated] - human

N;Alternate names: apoA-I-2; apoA-I-4; preproapoA-I; prostacyclin stabilizing factor  
C;Species: Homo sapiens (man)

C;Date: 14-Nov-1983 #sequence revision 14-Nov-1983 #text change 09-Jul-2004

C;Accession: A90947; B90947; S02373; A93465; A21147; A93519; B93519; A93472; A94010; A216197

R;Seilhamer, J.J.; Protter, A.A.; Frossard, P.; Levy-Wilson, B.

DNA 3, 309-317, 1984

A;Title: Isolation and DNA sequence of full-length cDNA and of the entire gene for human  
A;Reference number: A90947; MUID:85026665; PMID:6207999

A;Accession: A90947

A;Molecule type: DNA

A;Residues: 1-267 <SE1>

A;Cross-references: UNIPROT:P02647; UNIPARC:UPI000002C911; GB:X01038; NID:g28769; PIDN:C

A;Accession: B90947

A;Molecule type: mRNA

A;Residues: 1-267 <SE2>

A;Cross-references: UNIPARC:UPI000002C911; GB:X01038; NID:g28769; PIDN:CAA25519.1; PID:g  
R;Makrides, S.C.; Ruiz-Opazo, N.; Hayden, M.; Nussbaum, A.L.; Breslow, J.L.; Zannis, V.I

Eur. J. Biochem. 173, 465-471, 1988

A;Title: Sequence and expression of Tangier apoA-I gene.

A;Reference number: S02373; MUID:88196137; PMID:3129297

A;Accession: S02373

A;Molecule type: DNA

A;Residues: 1-267 <MAK>

A;Cross-references: UNIPARC:UPI000002C911; EMBL:X07496; NID:g28774; PIDN:CAA30377.1; PID  
R;Shoulders, C.C.; Kornblihtt, A.R.; Munro, B.S.; Baralle, F.E.

Nucleic Acids Res. 11, 2827-2837, 1983

A;Title: Gene structure of human apolipoprotein AI.

A;Reference number: A93465; MUID:83220822; PMID:6406984

A;Accession: A93465

A;Molecule type: DNA

A;Residues: 1-267 <SHO>

A;Cross-references: UNIPARC:UPI000002C911; GB:J00098; GB:J00099; GB:J00100; GB:J00101; G  
R;Karathanasis, S.K.; Zannis, V.I.; Breslow, J.L.

Proc. Natl. Acad. Sci. U.S.A. 80, 6147-6151, 1983

A;Title: Isolation and characterization of the human apolipoprotein A-I gene.

A;Reference number: A21147; MUID:84016011; PMID:6413973

A;Accession: A21147

A;Molecule type: DNA

A;Residues: 1-267 <KAR>

A;Cross-references: UNIPARC:UPI000002C911; GB:J00098; GB:J03222; NID:g178765; PIDN:AAB59  
R;Sharpe, C.R.; Sidoli, A.; Shelley, C.S.; Lucero, M.A.; Shoulders, C.C.; Baralle, F.E.

Nucleic Acids Res. 12, 3917-3932, 1984

A;Title: Human apolipoproteins AI, AII, CII and CIII. cDNA sequences and mRNA abundance.

A;Reference number: A93519; MUID:84221405; PMID:6328445

A;Accession: A93519

A;Molecule type: mRNA

A;Residues: 1-267 <SHA>

A;Cross-references: UNIPARC:UPI000002C911; GB:X00566; NID:g28765; PIDN:CAA25232.1; PID:g

A;Accession: B93519  
A;Molecule type: DNA  
A;Residues: 1-24 <SH2>  
A;Cross-references: UNIPARC:UPI0000174019  
R;Cheung, P.; Chan, L.  
Nucleic Acids Res. 11, 3703-3715, 1983  
A;Title: Nucleotide sequence of cloned cDNA of human apolipoprotein A-I.  
A;Reference number: A93472; MUID:83220772; PMID:6304641  
A;Accession: A93472  
A;Molecule type: mRNA  
A;Residues: 1-267 <CHE>  
A;Cross-references: UNIPARC:UPI000002C911; GB:J00098; GB:J00100; GB:J00101; GB:J00102  
R;Law, S.W.; Brewer Jr., H.B.  
Proc. Natl. Acad. Sci. U.S.A. 81, 66-70, 1984  
A;Title: Nucleotide sequence and the encoded amino acids of human apolipoprotein A-I mRNA  
A;Reference number: A94010; MUID:84119464; PMID:6198645  
A;Accession: A94010  
A;Molecule type: mRNA  
A;Residues: 1-267 <LAW>  
A;Cross-references: UNIPARC:UPI000002C911; GB:J00098; GB:J00100; GB:J00101; GB:J00102  
R;Zannis, V.I.; Karathanasis, S.K.; Keutmann, H.T.; Goldberger, G.; Breslow, J.L.  
Proc. Natl. Acad. Sci. U.S.A. 80, 2574-2578, 1983  
A;Title: Intracellular and extracellular processing of human apolipoprotein A-I: secreted  
A;Reference number: A21118; MUID:83195100; PMID:6405383  
A;Accession: A21118  
A;Molecule type: protein  
A;Residues: 1-24 <ZAN>  
A;Cross-references: UNIPARC:UPI0000174019  
R;Brewer Jr., H.B.; Fairwell, T.; Kay, L.; Meng, M.; Ronan, R.; Law, S.; Light, J.A.  
Biochem. Biophys. Res. Commun. 113, 626-632, 1983  
A;Title: Human plasma preapoA-I: isolation and amino-terminal sequence.  
A;Reference number: A90112; MUID:83256553; PMID:6409108  
A;Accession: A90112  
A;Molecule type: protein  
A;Residues: 19-27 <BRE>  
A;Cross-references: UNIPARC:UPI000017401A  
R;Brewer Jr., H.B.; Fairwell, T.; LaRue, A.; Ronan, R.; Houser, A.; Bronzert, T.J.  
Biochem. Biophys. Res. Commun. 80, 623-630, 1978  
A;Title: The amino acid sequence of human APOA-I, an apolipoprotein isolated from high density lipoproteins  
A;Reference number: A90209; MUID:78123731; PMID:204308  
A;Accession: A90209  
A;Molecule type: protein  
A;Residues: 25-57,'Q',59-169,'QQ',172-267 <BR2>  
A;Cross-references: UNIPARC:UPI000017401B  
R;Yui, Y.; Aoyama, T.; Morishita, H.; Takahashi, M.; Takatsu, Y.; Kawai, C.  
J. Clin. Invest. 82, 803-807, 1988  
A;Title: Serum prostacyclin stabilizing factor is identical to apolipoprotein A-I (Apo A-I)  
A;Reference number: A30516; MUID:88331387; PMID:3047170  
A;Accession: A30516  
A;Molecule type: protein  
A;Residues: 25-56 <YUI>  
A;Cross-references: UNIPARC:UPI000017401C  
R;Nichols, W.C.; Dwulet, F.E.; Liepnies, J.; Benson, M.D.  
Biochem. Biophys. Res. Commun. 156, 762-768, 1988  
A;Title: Variant apolipoprotein AI as a major constituent of a human hereditary amyloid.  
A;Reference number: A31582; MUID:89050104; PMID:3142462  
A;Accession: A31582  
A;Molecule type: protein  
A;Residues: 25-49,'R',51-85,'D',87-107 <NIC>  
A;Cross-references: UNIPARC:UPI000017401D  
A;Note: variant sequence from patient with familial amyloidotic polyneuropathy type III  
R;Manjunath, P.; Marcel, Y.L.; Uma, J.; Seidah, N.G.; Chretien, M.; Chapdelaine, A.  
J. Biol. Chem. 264, 16853-16857, 1989  
A;Title: Apolipoprotein A-I binds to a family of bovine seminal plasma proteins.  
A;Reference number: A34409; MUID:89380318; PMID:2506184  
A;Accession: A34409  
A;Molecule type: protein  
A;Residues: 25-48 <MAN>  
A;Cross-references: UNIPARC:UPI000017401E  
R;Stoffel, W.; Binczek, E.  
Biol. Chem. Hoppe-Seyler 369, 1055-1063, 1988  
A;Title: Structural requirements of human preproapolipoprotein AI for translocation and secretion  
A;Reference number: S02737; MUID:89149957; PMID:3228490

A;Accession: S02737  
A;Status: not compared with conceptual translation  
A;Molecule type: mRNA  
A;Residues: 1-6,'AV',9,'LV',12-29 <STO>  
A;Cross-references: UNIPARC:UPI000017401F  
A;Note: part of this sequence, including the amino end of the mature protein, was confirmed by sequencing  
R;Stoffel, W.; Binczek, E.  
Biol. Chem. Hoppe-Seyler 372, 481-488, 1991  
A;Title: Transient expression of wild type and mutant human apolipoprotein AI in COS cells  
A;Reference number: S16197; MUID:92029676; PMID:1930731  
A;Contents: annotation; extension of studies in reference S02737  
R;Stoffel, W.; Kruger, E.; Deutzmann, R.  
Hoppe-Seyler's Z. Physiol. Chem. 364, 227-237, 1983  
A;Title: Cell-free translation of human liver apolipoprotein AI and AII mRNA processing  
A;Reference number: A19913; MUID:83236195; PMID:6407957  
A;Accession: B19913  
A;Molecule type: protein  
A;Residues: 1-6,'X',8-13,'XX',17-18,'XX',21,'X',23-25,'X',27-29 <ST2>  
A;Cross-references: UNIPARC:UPI0000174020  
R;Enholm, C.; Bozas, S.E.; Tenkanen, H.; Kirszbaum, L.; Metso, J.; Murphy, B.; Walker, B.  
Biochim. Biophys. Acta 1086, 255-260, 1991  
A;Title: The apolipoprotein A-I binding protein of placenta and the SP-40,40 protein of human liver  
A;Reference number: A56815; MUID:92075698; PMID:1742316  
A;Accession: A56815  
A;Molecule type: protein  
A;Residues: 25-31,'P',33 <EHN>  
A;Cross-references: UNIPARC:UPI000006D38A  
A;Experimental source: serum  
A;Note: sequence extracted from NCBI backbone (NCBIP:69759)  
R;Kunitake, S.T.; Carilli, C.T.; Lau, K.; Protter, A.A.; Naya-Vigne, J.; Kane, J.P.  
Biochemistry 33, 1988-1993, 1994  
A;Title: Identification of proteins associated with apolipoprotein A-I-containing lipoproteins  
A;Reference number: A54223; MUID:94162201; PMID:8117655  
A;Accession: A54223  
A;Molecule type: protein  
A;Residues: 25-39 <KUN>  
A;Cross-references: UNIPARC:UPI0000174021  
R;Mogulilevsky, N.; Roobol, C.; Loriau, R.; Guillaume, J.P.; Jacobs, P.; Cravador, A.; Heinecke  
DNA 8, 429-436, 1989  
A;Title: Production of human recombinant proapolipoprotein A-I in Escherichia coli: purification and characterization  
A;Reference number: I39476; MUID:89377481; PMID:2673706  
A;Accession: I39476  
A;Molecule type: mRNA  
A;Residues: 19-267 <RES>  
A;Cross-references: UNIPARC:UPI0000000473; GB:M29068; NID:g178774; PIDN:AAA51747.1; PIDN:AAA51748.1  
R;Higuchi, K.; Law, S.W.; Hoeg, J.M.; Schumacher, U.K.; Meglin, N.; Brewer, H.B.  
J. Biol. Chem. 263, 18530-18536, 1988  
A;Title: Tissue-specific expression of apolipoprotein A-I (ApoA-I) is regulated by the 5' noncoding region  
A;Reference number: I39475; MUID:89054040; PMID:3142880  
A;Accession: I39475  
A;Molecule type: DNA  
A;Residues: 1-14 <RE2>  
A;Cross-references: UNIPARC:UPI0000000391; GB:J04066; NID:g178763; PIDN:AAA51746.1; PIDN:AAA51747.1  
R;Breslow, J.L.  
Annu. Rev. Biochem. 54, 699-727, 1985  
A;Title: Human apolipoprotein molecular biology and genetic variation.  
A;Reference number: A90042; MUID:85278004; PMID:3896129  
A;Contents: annotation; review of sequences, variants and gene location  
R;Hoeg, J.M.; Meng, M.S.; Ronan, R.; Fairwell, T.; Brewer Jr., H.B.  
J. Biol. Chem. 261, 3911-3914, 1986  
A;Title: Human apolipoprotein A-I. Post-translational modification by fatty acid acylation  
A;Reference number: A92577; MUID:86140194; PMID:3005308  
A;Contents: annotation; acylation with palmitate  
A;Note: an undetermined serine or threonine is acylated by fatty acid; the acylating fatty acid is not specified  
R;Law, S.W.; Brewer, H.B.  
J. Biol. Chem. 260, 12810-12814, 1985  
A;Title: Tangier disease: The complete mRNA sequence encoding for preproapo-A-I.  
A;Reference number: I55236; MUID:86008382; PMID:2995392  
A;Accession: I55236  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-143,'D',145-267 <RE3>





Db	121	VQPYLDDDFQKQWQEE	MELYRQKV	EPLRAELH	EGTRQK	LHELHEK	LSP	LGEEV	DRARA	HV	180
QY	181	DALRTHLAPYSDEL	RQRLAAR	LEALKENG	GARLA	EYHAKA	TEHLST	LSEKAK	PALED	LRQ	240
Db	181	DALRTHLAPYSDEL	RQRLAAR	LEALKENG	GARLA	EYHAKA	SEHLST	LSEKAK	PALED	LRQ	240
QY	241	GLLPVLESFKVSFL	SAL	EYTKKL	NTQ						267
Db	241	GLLPVLESFKVSFL	SAL	EYTKKL	STQ						267

RESULT 4  
LPGAL  
apolipoprotein A-I precursor - dog  
CSpecies: Canis lupus familiaris (dog)  
CDate: 17-Dec-1982 #sequence\_revision 14-Jul-1994 #text\_change 09-Jul-2004  
CAccession: A60940; A03092; A61418  
R.Luo, C.C.; Li, W.H.; Chan, L.  
J. Lipid Res. 30, 1735-1746, 1989  
ATitle: Structure and expression of dog apolipoprotein A-I, E, and C-I mRNAs: implications  
AReference number: A60940; MUID:90132271; PMID:2515239  
AAccession: A60940  
AMolecule type: mRNA  
AResidues: 1-266 <LUO>  
ACross-references: UNIPROT:P02648; UNIPARC:UPI00000125BD7  
R; Chung, H.; Randolph, A.; Reardon, I.; Heinrikson, R.L.  
J. Biol. Chem. 257, 2961-2967, 1982  
ATitle: The covalent structure of apolipoprotein A-I from canine high density lipoproteins  
AReference number: A03092; MUID:82142425; PMID:6801039  
AAccession: A03092  
AMolecule type: protein  
AResidues: 25-167, 'G', 169-201, 'Q', 203-234, 'Q', 236-266 <CHU>  
ACross-references: UNIPARC:UPI0000174023  
R; Nakai, T.; Whayne, T.F.; Tang, J.  
FEBS Lett. 64, 409-411, 1976  
ATitle: The amino- and carboxyl-terminal sequences of canine apolipoprotein A-I.  
AReference number: A61418; MUID:76210910; PMID:179887  
AAccession: A61418  
AMolecule type: protein  
AResidues: 25-56, 'Z', 261-262, 'A' <NAK>  
ACross-references: UNIPARC:UPI0000174024; UNIPARC:UPI0000174025  
CSuperfamily: apolipoprotein A-I  
CKeywords: atherosclerosis; cholesterol metabolism; HDL; intestine; lipid transport; lipoprotein  
F.1-18/Domain: signal sequence #status predicted <SIG>  
F.19-24/Domain: propeptide #status predicted <PRO>  
F.25-266/Product: apolipoprotein A-I #status experimental <MAT>

	Query Match	85.3%;	Score 1161.5;	DB 1;	Length 266;
	Best Local Similarity	85.0%;	Pred. No. 9.9e-59;		
	Matches 227;	Conservative 19;	Mismatches 20;	Indels 1;	Gaps 14;
Qy	1	MKAAVLTLAVFLTGSQAARHFQQDEPPQPSPWDRVKDLATVYVDLVLKDSGRDYVSQFEFS	60		
Dd	1	MKAALLTLAVFLTGSQAARHFQQDE-PQSPWDRVKDLATVYVDVAVKDSGRDYYAQQFEAS	59		
Qy	61	ALGKQLNLKLNDNWDSVTSFSLREQLGPVTQEFWDNLEKETEGLRQEEMSKDLEEVRKAK	120		
Dd	60	ALGKQLNLKLNDNWDLSSTVTKLREQIGPVTQEFWDNLEKETEVRLRQEEMSKDLEEVRKKQ	119		
Qy	121	VQPYLDDFKKWQEEMLSYTRQKVPEPLRAELQEGARQKLHELOEKLSPLGSEMRDRARAHV	180		
Dd	120	VQPYLDDFKKWQEEVELYRQKVAPGLSELREGARQKLQELQEKLSPLAEELRDRAETHV	179		
Qy	181	DALRTHLPAYSDELQRLLAARLEALKENGGARLAELYHAKATEHLSTLSEKAKPALEDLRQ	240		
Dd	180	DALRAOLAPYSDDLRRERLAARLEALKKEGGGASLAELYHARASEOISALGEKARPAAEDLRQ	239		

**QY**      241 GLLPVLESFKVSFLSALEEYTKLNTQ 267  
         |||||  
**Dd**      240 GLLPVLESFKVSLAIDENYTKLNQAQ 266  
         ||||| : : : : :

## RESULT 5

Db 60 ALGKHLNLKLLDNWDSLGSTFTKVRQLGPVTQEFWDLNLEKETEALRQEMSKDLEEVKKK 119

Qy 121 VQPYLDDFQKKWQEEEMELYRQKVEPLRAELQEGARQKLHELQEKLSPLGEEMRDRARAHV 180

Db 120 VQPYLDDFQNKWQEEEMETRYQKMAPLGAEFREGARQKVQELQEKLSPLAEELRDRLRRAHV 179

Qy 181 DALRTHLAPYSDELQRLAARLEALKENGGARLAEYHAKATEHLSTLSEKAKPALEDLRQ 240

Db 180 EALRQQLAPYSDDLQRMAARFEALKEGGGS-LAEYQAKAQEQLKALGEKAKPALEDLRQ 238

Qy 241 GLLPVLESFKVSFLSALAEYTKKLNQ 267

Db 239 GLLPVLENLKVSILAAIDEASKKLNQ 265

RESULT 7

JT0672

apolipoprotein A-I - pig

N;Alternate names: apo-A-I

C;Species: Sus scrofa domestica (domestic pig)

C;Date: 28-Oct-1994 #sequence revision 28-Oct-1994 #text\_change 09-Jul-2004

C;Accession: JT0672; FN0471; A05311

R;Trieu, V.N.; Patel, B.; Zhan, R.; Black, D.D.

Gene 134, 267-270, 1993

A;Title: Sequence of the porcine apoA-I gene.

A;Reference number: JT0672; MUID:94085789; PMID:7916724

A;Accession: JT0672

A;Molecule type: DNA

A;Residues: 1-265 <TRI>

A;Cross-references: UNIPROT:P18648; UNIPARC:UPI000017779E; EMBL:Z14124; NID:g1893

A;Note: this translation is not annotated in GenBank entry SSAPOAIG, release 111.0; the

R;Trieu, V.N.; Hasler-Rapacz, J.; Rapacz, J.; Black, D.D.

Gene 123, 173-179, 1993

A;Title: Sequences and expression of the porcine apolipoprotein A-I and C-III mRNAs.

A;Reference number: FN0471; MUID:93154581; PMID:8428656

A;Accession: FN0471

A;Molecule type: mRNA

A;Residues: 105-265 <TR2>

A;Cross-references: UNIPARC:UPI000017779F

A;Experimental source: liver

R;Mahley, R.W.; Weisgraber, K.H.; Innerarity, T.; Brewer Jr., H.B.

Biochemistry 15, 1928-1933, 1976

A;Title: Characterization of the plasma lipoproteins and apoproteins of the Erythrocebus

A;Reference number: A90395; MUID:76184721; PMID:178359

A;Accession: A05311

A;Molecule type: protein

A;Residues: 25-34 <MAH>

A;Cross-references: UNIPARC:UPI00001777A0

C;Comment: This protein is the major apolipoprotein of high-density lipoprotein and serv

C;Genetics:

A;Gene: apoA-I

A;Introns: 15/1; 66/2

C;Superfamily: apolipoprotein A-I

C;Keywords: cholesterol metabolism; HDL; intestine; lipid binding; lipid metabolism; lip

F;99/Region: ochre stop codon

Query Match 80.2%; Score 1093; DB 2; Length 265;

Best Local Similarity 80.1%; Pred. No. 7.1e-55;

Matches 214; Conservative 20; Mismatches 31; Indels 2; Gaps 2;

Qy 1 MKA AVLTLAVLFLTGSQARHFQQDEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGS 60

Db 1 MKA AVLTLAVLFLTGSQARHFQQDD-PQSPWDRVKDFATVYVDAIKDSGRDYVAQFEAS 59

Qy 61 ALGKQLNLKLLDNWDSVTSTFSKRLREQLGPVTQEFWDLNLEKETEGRLQEMSKDLEEVKAK 120

Db 60 ALGKHLKLLDNWDSLGSTFTKVRQLGPVTQEFWDLNLEKETEGRLQEMSKDLEEVKKK 119

Qy 121 VQPYLDDFQKKWQEEEMELYRQKVEPLRAELQEGARQKLHELQEKLSPLGEEMRDRARAHV 180

Db 120 VQPYLDDFQNKWQEEEMETRYQKMAPLGAEFREGARQKVQELQEKLSPLAEELRDRLRRAHV 178

Qy 181 DALRTHLAPYSDELQRLAARLEALKENGGARLAEYHAKATEHLSTLSEKAKPALEDLRQ 240

Db 179 AALRQHVPAPYSDDLQRMAARFEALKE-GGDSLAEYQAKAQEQLKALGEKAKPALEDLRQ 237

Qy 241 GLLPVLESFKVSFLSALAEYTKKLNQ 267

Db 238 GLLPVLENLKVSILAAIDEASKKLNQ 264

RESULT 9

LPRB1B

apolipoprotein A-I precursor (clone PRBA-502) - rabbit

C;Species: Oryctolagus cuniculus (domestic rabbit)

C;Date: 31-Dec-1990 #sequence\_revision 31-Dec-1990 #text\_change 22-Jun-1999

C;Accession: S00230; S20557

R;Pan, T.C.; Hao, Q.L.; Yamin, T.T.; Dai, P.H.; Chen, B.S.; Chen, S.L.; Kroon, P.A.; Cha

Eur. J. Biochem. 170, 99-104, 1987

A;Title: Rabbit apolipoprotein A-I mRNA and gene. Evidence that rabbit apolipoprotein A-

A;Reference number: S00230; MUID:88082866; PMID:3121329

A;Accession: S00230

A;Molecule type: mRNA

A;Residues: 1-265 <PAN>

A;Cross-references: UNIPARC:UPI000016C53A; EMBL:X06658; NID:g1461; PIDN:CAA29857.1; PID:

A;Note: the authors translated the codon AGC for residue 174 as Arg

A;Accession: S20557

A;Molecule type: DNA

A;Residues: 1-17, 'R', 19-44, 'I', 46-122, 'Y', 124-146, 'V', 148-265 <PAN2>

A;Cross-references: UNIPARC:UPI000016C539; EMBL:X06659; NID:g1459; PIDN:CAA29858.1; PID:

C;Comment: This protein is synthesized in the small intestine.

C;Comment: This protein is a major component of the high density lipoproteins in plasma.

C;Genetics:

A;Introns: 15/1; 66/2

Db 180 EALRQHVPAPYSDDLQRMAARFEALKEGGGS-LAEYQAKAQEQLKALGEKAKPALEDLRQ 238

Qy 241 GLLPVLESFKVSFLSALAEYTKKLNQ 267

Db 239 GLLPVLENLKVSILAAIDEASKKLNQ 265

RESULT 8

S31394

apolipoprotein A-I - pig

C;Species: Sus scrofa domestica (domestic pig)

C;Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 09-Jul-2004

C;Accession: S31394

R;Moechel, B.; Flach, R.; Weiss, B.; Weiler-Guettler, H.; Frey, A.; Zinke, H.; Gassen, H

submitted to the EMBL Data Library, November 1992

A;Description: Genomic organization of the porcine apolipoprotein A1 gene and study of g

A;Reference number: S31394

A;Accession: S31394

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-264 <MOE>

A;Cross-references: UNIPROT:P18648; UNIPARC:UPI000016C68A; EMBL:X69477; NID:g1889; PIDN:

C;Superfamily: apolipoprotein A-I

Query Match 79.8%; Score 1087.5; DB 2; Length 264;

Best Local Similarity 80.9%; Pred. No. 1.4e-54;

Matches 216; Conservative 18; Mismatches 30; Indels 3; Gaps 3;

Qy 1 MKA AVLTLAVLFLTGSQARHFQQDEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGS 60

Db 1 MKA AVLTLAVLFLTGSQARHFQQDD-PQSPWDRVKDFATVYVDAIKDSGRDYVAQFEAS 59

Qy 61 ALGKQLNLKLLDNWDSVTSTFSKRLREQLGPVTQEFWDLNLEKETEGRLQEMSKDLEEVKAK 120

Db 60 ALGKHLNLKLLDNWDSLGSTFTKVRQLGPVTQEFWDLNLEKETEGRLQEMSKDLEEVKKK 119

Qy 121 VQPYLDDFQKKWQEEEMELYRQKVEPLRAELQEGARQKLHELQEKLSPLGEEMRDRARAHV 180

Db 120 VQPYLDDFQNKWQEEEMETRYQKMAPLGAEFREGARQKVQELQEKLSPLAEELRDRLRRAHV 178

Qy 181 DALRTHLAPYSDELQRLAARLEALKENGGARLAEYHAKATEHLSTLSEKAKPALEDLRQ 240

Db 179 AALRQHVPAPYSDDLQRMAARFEALKE-GGDSLAEYQAKAQEQLKALGEKAKPALEDLRQ 237

Qy 241 GLLPVLESFKVSFLSALAEYTKKLNQ 267

Db 238 GLLPVLENLKVSILAAIDEASKKLNQ 264

RESULT 9

LPRB1B

apolipoprotein A-I precursor (clone PRBA-502) - rabbit

C;Species: Oryctolagus cuniculus (domestic rabbit)

C;Date: 31-Dec-1990 #sequence\_revision 31-Dec-1990 #text\_change 22-Jun-1999

C;Accession: S00230; S20557

R;Pan, T.C.; Hao, Q.L.; Yamin, T.T.; Dai, P.H.; Chen, B.S.; Chen, S.L.; Kroon, P.A.; Cha

Eur. J. Biochem. 170, 99-104, 1987

A;Title: Rabbit apolipoprotein A-I mRNA and gene. Evidence that rabbit apolipoprotein A-

A;Reference number: S00230; MUID:88082866; PMID:3121329

A;Accession: S00230

A;Molecule type: mRNA

A;Residues: 1-265 <PAN>

A;Cross-references: UNIPARC:UPI000016C53A; EMBL:X06658; NID:g1461; PIDN:CAA29857.1; PID:

A;Note: the authors translated the codon AGC for residue 174 as Arg

A;Accession: S20557

A;Molecule type: DNA

A;Residues: 1-17, 'R', 19-44, 'I', 46-122, 'Y', 124-146, 'V', 148-265 <PAN2>

A;Cross-references: UNIPARC:UPI000016C539; EMBL:X06659; NID:g1459; PIDN:CAA29858.1; PID:

C;Comment: This protein is synthesized in the small intestine.

C;Comment: This protein is a major component of the high density lipoproteins in plasma.

C;Genetics:

A;Introns: 15/1; 66/2











GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 28, 2006, 20:39:08 ; Search time 163 Seconds  
(without alignments)  
684.420 Million cell updates/sec

Title: US-09-803-918A-2  
Perfect score: 1362  
Sequence: 1 MKAAVLTIAVLFLTGSQARH.....SFKVSFLSALEYTKKLNQ 267

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA Main:  
1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep:\*  
2: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep:\*  
3: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep:\*  
4: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep:\*  
5: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep:\*  
6: /cgn2\_6/ptodata/1/pubpaa/US11\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Length	DB ID	Description
1	1362	100.0	267	3	US-09-803-918A-2 Sequence 2, Appli
2	1362	100.0	267	3	US-09-803-918A-2 Sequence 15, Appl
3	1362	100.0	267	3	US-09-803-918A-2 Sequence 30, Appl
4	1362	100.0	267	4	US-10-032-189-75 Sequence 75, Appl
5	1362	100.0	267	4	US-10-283-599-260 Sequence 260, App
6	1362	100.0	267	4	US-10-403-902A-30 Sequence 30, Appl
7	1362	100.0	267	4	US-10-186-288-10 Sequence 10, Appl
8	1362	100.0	267	4	US-10-038-854-219 Sequence 219, App
9	1362	100.0	267	4	US-10-038-854-226 Sequence 226, App
10	1362	100.0	267	5	US-10-991-217-260 Sequence 260, App
11	1362	100.0	267	5	US-10-987-454-2 Sequence 2, Appli
12	1362	100.0	267	6	US-11-017-037-15 Sequence 15, Appl
13	1362	100.0	267	6	US-11-019-829-15 Sequence 15, Appl
14	1362	100.0	267	6	US-11-017-059-15 Sequence 15, Appl
15	1362	100.0	275	5	US-10-852-705A-4 Sequence 4, Appli
16	1359	99.8	267	4	US-10-032-189-74 Sequence 74, Appl
17	1359	99.8	267	4	US-10-408-765A-253 Sequence 253, App
18	1346	98.8	267	3	US-09-919-039-27 Sequence 27, Appl
19	1306	95.9	267	3	US-09-987-107-16 Sequence 16, Appl
20	1306	95.9	267	4	US-10-032-189-77 Sequence 77, Appl
21	1306	95.9	267	4	US-10-038-854-223 Sequence 223, App
22	1306	95.9	267	4	US-10-038-854-230 Sequence 230, App
23	1306	95.9	267	5	US-10-987-454-18 Sequence 18, Appl
24	1306	95.9	267	5	US-10-987-454-23 Sequence 23, Appl
25	1306	95.9	267	6	US-11-017-037-16 Sequence 16, Appl
26	1306	95.9	267	6	US-11-017-059-16 Sequence 16, Appl
27	1299	95.4	267	4	US-10-032-189-78 Sequence 78, Appl

28	1286	94.4	276	5	US-10-987-454-199 Sequence 199, App
29	1286	94.4	518	5	US-10-987-454-160 Sequence 160, App
30	1286	94.4	518	5	US-10-987-454-170 Sequence 170, App
31	1285	94.3	524	5	US-10-987-454-203 Sequence 203, App
32	1285	94.3	526	5	US-10-987-454-207 Sequence 207, App
33	1285	94.3	528	5	US-10-987-454-212 Sequence 212, App
34	1285	94.3	530	5	US-10-987-454-216 Sequence 216, App
35	1284	94.3	462	5	US-10-987-454-194 Sequence 194, App
36	1284	94.3	562	5	US-10-987-454-221 Sequence 221, App
37	1284	94.3	566	5	US-10-987-454-229 Sequence 229, App
38	1282	94.1	424	5	US-10-987-454-181 Sequence 181, App
39	1282	94.1	666	5	US-10-987-454-156 Sequence 156, App
40	1281	94.1	249	4	US-10-032-189-76 Sequence 76, Appl
41	1281	94.1	249	4	US-10-038-854-220 Sequence 220, App
42	1281	94.1	249	4	US-10-038-854-227 Sequence 227, App
43	1281	94.1	251	5	US-10-987-454-176 Sequence 176, App
44	1281	94.1	464	5	US-10-987-454-185 Sequence 185, App
45	1281	94.1	493	5	US-10-987-454-151 Sequence 151, App

ALIGNMENTS

RESULT 1  
US-09-803-918A-2  
; Sequence 2, Application US/09803918A  
; Patent No. US20020064820A1  
; GENERAL INFORMATION:  
; APPLICANT: Dayer, Jean-Michel  
; APPLICANT: Burger, Danielle  
; APPLICANT: Kohno, Tadahiko  
; APPLICANT: Edwards III, Carl K.  
; TITLE OF INVENTION: APO-A-1 REGULATION OF T-CELL SIGNALING  
; FILE REFERENCE: 06843.0035-00000  
; CURRENT APPLICATION NUMBER: US/09/803,918A  
; CURRENT FILING DATE: 2001-07-19  
; PRIOR APPLICATION NUMBER: 60/189,008  
; PRIOR FILING DATE: 2000-03-13  
; PRIOR APPLICATION NUMBER: 60/193,551  
; PRIOR FILING DATE: 2000-03-31  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 267  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-803-918A-2

Query Match	100.0%;	Score 1362;	DB 3;	Length 267;
Best Local Similarity	100.0%;	Pred. No. 1e-92;		
Matches	267;	Conservative	0;	Mismatches 0; Indels 0; Gaps 0;
QY	1	MKAAVLTIAVLFLTGSQARHFQQDEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGS	60	
Db	1	MKAAVLTIAVLFLTGSQARHFQQDEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGS	60	
QY	61	ALGKQLNLKLLDNWDSVTSTFSKLRQQLGPVTQBFWDNLEKETETGLRQEMSKDLEEVKAK	120	
Db	61	ALGKQLNLKLLDNWDSVTSTFSKLRQQLGPVTQBFWDNLEKETETGLRQEMSKDLEEVKAK	120	
QY	121	VQPYLDDFQKKWQEMELYRQKVEPLRAELQEGARQKLHELQEKLSPLGEMDRARAHV	180	
Db	121	VQPYLDDFQKKWQEMELYRQKVEPLRAELQEGARQKLHELQEKLSPLGEMDRARAHV	180	
QY	181	DALRTHLAPYSDELQRLAARLEALKENGARLAAYHAKATEHLSTLSEKAKPALEDLRQ	240	
Db	181	DALRTHLAPYSDELQRLAARLEALKENGARLAAYHAKATEHLSTLSEKAKPALEDLRQ	240	
QY	241	GLLPVLESFKVSFLSALEYTKKLNQ	267	
Db	241	GLLPVLESFKVSFLSALEYTKKLNQ	267	

```
RESULT 2
US-09-987-107-15
; Sequence 15, Application US/09987107
; Patent No. US20020156007A1
; GENERAL INFORMATION:
; APPLICANT: GRAVERSEN, Jonas
; APPLICANT: MOESTRUP, Soren
; TITLE OF INVENTION: APOLIPROTEINS ANALOGUES
; FILE REFERENCE: GRAVERSENIA
; CURRENT APPLICATION NUMBER: US/09/987,107
; CURRENT FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/264,022
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: DK PA2001 00057
; PRIOR FILING DATE: 2001-01-15
; PRIOR APPLICATION NUMBER: DK PA2000 01682
; PRIOR FILING DATE: 2000-11-10
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 267
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-987-107-15

Query Match      100.0%; Score 1362; DB 3; Length 267;
Best Local Similarity 100.0%; Pred. No. 1e-92;
Matches 267; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MKAAVLT LAVLFLTG SQARHFQQDEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGS 60
Db      1 MKAAVLT LAVLFLTG SQARHFQQDEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGS 60

QY      61 ALGKQLNLKLLDNWDSVTSTFSKLRQGLGPVTQEFWDNLEKETETGLRQEMSKDLEEVKAK 120
Db      61 ALGKQLNLKLLDNWDSVTSTFSKLRQGLGPVTQEFWDNLEKETETGLRQEMSKDLEEVKAK 120

QY      121 VQPYLDDFQKKWQEEMELYRQKVEPLRAELQEGARQKLHELQEKLSPLGEEMRDRARAHV 180
Db      121 VQPYLDDFQKKWQEEMELYRQKVEPLRAELQEGARQKLHELQEKLSPLGEEMRDRARAHV 180

QY      181 DALRTHLAPYSDELQRRLAARLEALKENGARLAEYHAKATEHLSTLSEKAKPALEDLRQ 240
Db      181 DALRTHLAPYSDELQRRLAARLEALKENGARLAEYHAKATEHLSTLSEKAKPALEDLRQ 240

QY      241 GLLPVLESFKVSFLSALEEYTKKLNTQ 267
Db      241 GLLPVLESFKVSFLSALEEYTKKLNTQ 267

RESULT 3
US-09-802-640-30
; Sequence 30, Application US/09802640
; Publication No. US20030036057A1
; GENERAL INFORMATION:
; APPLICANT: Braun, Andreas
; APPLICANT: Bonsal Aruna
; APPLICANT: Kleyn Patrick
; TITLE OF INVENTION: GENES AND POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISEASE AND THEIR USE
; FILE REFERENCE: 24736-2048
; CURRENT APPLICATION NUMBER: US/09/802,640
; CURRENT FILING DATE: 2001-03-09
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 267
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-802-640-30

Query Match      100.0%; Score 1362; DB 3; Length 267;
Best Local Similarity 100.0%; Pred. No. 1e-92;
```

```
Matches 267; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MKAAVLT LAVLFLTG SQARHFQQDEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGS 60
Db      1 MKAAVLT LAVLFLTG SQARHFQQDEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGS 60

QY      61 ALGKQLNLKLLDNWDSVTSTFSKLRQGLGPVTQEFWDNLEKETETGLRQEMSKDLEEVKAK 120
Db      61 ALGKQLNLKLLDNWDSVTSTFSKLRQGLGPVTQEFWDNLEKETETGLRQEMSKDLEEVKAK 120

QY      121 VQPYLDDFQKKWQEEMELYRQKVEPLRAELQEGARQKLHELQEKLSPLGEEMRDRARAHV 180
Db      121 VQPYLDDFQKKWQEEMELYRQKVEPLRAELQEGARQKLHELQEKLSPLGEEMRDRARAHV 180

QY      181 DALRTHLAPYSDELQRRLAARLEALKENGARLAEYHAKATEHLSTLSEKAKPALEDLRQ 240
Db      181 DALRTHLAPYSDELQRRLAARLEALKENGARLAEYHAKATEHLSTLSEKAKPALEDLRQ 240

QY      241 GLLPVLESFKVSFLSALEEYTKKLNTQ 267
Db      241 GLLPVLESFKVSFLSALEEYTKKLNTQ 267

RESULT 4
US-10-032-189-75
; Sequence 75, Application US/10032189
; Publication No. US20030170630A1
; GENERAL INFORMATION:
; APPLICANT: Alsobrook II, John P
; APPLICANT: Tchernev, Velizar T
; APPLICANT: Liu, Xiaohong
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Zerhusen, Bryan D
; APPLICANT: Patturajan, Meera
; APPLICANT: Grosse, William M
; APPLICANT: Lepley, Denise M
; APPLICANT: Burgess, Catherine E
; APPLICANT: Shimkets, Richard A
; APPLICANT: Grosse, William M
; APPLICANT: Szekeres, Edward S
; APPLICANT: Vernet, Corine A.M.
; APPLICANT: Li, Li
; APPLICANT: Casman, Stacie J
; APPLICANT: Boldog, Ferenc L
; APPLICANT: Gorman, Linda
; APPLICANT: Gangolli, Bsha A
; APPLICANT: Fernandes, Elma R
; APPLICANT: Rieger, Daniel K
; APPLICANT: Edinger, Shlomit R
; APPLICANT: Gunther, Erik
; APPLICANT: Millet, Isabelle
; APPLICANT: Sciore, Paul
; APPLICANT: Ellerman, Karen
; APPLICANT: MacDougall, John R
; APPLICANT: Smithson, Glennda
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-228
; CURRENT APPLICATION NUMBER: US/10/032,189
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 60/257,495
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: 60/258,171
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: 60/269,940
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: 60/274,192
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: 60/277,826
; PRIOR FILING DATE: 2001-03-22
; PRIOR APPLICATION NUMBER: 60/279,840
; PRIOR FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 60/282,981
; PRIOR FILING DATE: 2001-04-11
```



```
; PRIOR APPLICATION NUMBER: 60/283,656
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/309,247
; PRIOR FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: 60/311,754
; PRIOR FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: 60/313,331
; PRIOR FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 260
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 75
; LENGTH: 267
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-032-189-75

Query Match      100.0%; Score 1362; DB 4; Length 267;
Best Local Similarity 100.0%; Pred. No. 1e-92;
Matches 267; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MKAAVLTAVLFLTGSAQHFWQDEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGS 60
Db      1 MKAAVLTAVLFLTGSAQHFWQDEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGS 60

QY      61 ALGKQLNLKLLDNWDSVTSTFSKLRQGLPVTQEFWDNLEKETEGLRQEMSKDLEEVKAK 120
Db      61 ALGKQLNLKLLDNWDSVTSTFSKLRQGLPVTQEFWDNLEKETEGLRQEMSKDLEEVKAK 120

QY      121 VQPYLDDFQKKWQEEEMELYRQKVEPLRAELOEGARQKHLHELQEKLSPLGEEMRDRARAHV 180
Db      121 VQPYLDDFQKKWQEEEMELYRQKVEPLRAELOEGARQKHLHELQEKLSPLGEEMRDRARAHV 180

QY      181 DALRTHLAPYSDELRLQRLAARLEALKENGARLAEYHAKATEHLSTLSEKAKPALEDLRQ 240
Db      181 DALRTHLAPYSDELRLQRLAARLEALKENGARLAEYHAKATEHLSTLSEKAKPALEDLRQ 240

QY      241 GLLPVLESFKVSFLSALSEYTKKLNQ 267
Db      241 GLLPVLESFKVSFLSALSEYTKKLNQ 267

RESULT 5
US-10-283-599-260
; Sequence 260, Application US/10283599
; Publication No. US20030208059A1
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
; APPLICANT: Sekul, Renate
; APPLICANT: Buttner, Klaus
; APPLICANT: Cornut, Isabelle
; APPLICANT: Metz, Gunther
; APPLICANT: Dufourcq, Jean
; TITLE OF INVENTION: GENE THERAPY APPROACHES TO
; TITLE OF INVENTION: SUPPLY APOLIPOPROTEIN A-I AGONISTS AND THEIR
; TITLE OF INVENTION: USE TO TREAT DYSLIPIDEMIC DISORDERS.
; NUMBER OF SEQUENCES: 274
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/283,599
; FILING DATE: 29-OCT-2002
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
```

```
; APPLICATION NUMBER: 08/940,136
; FILING DATE: 29-SEP-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 009196-0007-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 260:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 267 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; US-10-283-599-260

Query Match      100.0%; Score 1362; DB 4; Length 267;
Best Local Similarity 100.0%; Pred. No. 1e-92;
Matches 267; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MKAAVLTAVLFLTGSAQHFWQDEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGS 60
Db      1 MKAAVLTAVLFLTGSAQHFWQDEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGS 60

QY      61 ALGKQLNLKLLDNWDSVTSTFSKLRQGLPVTQEFWDNLEKETEGLRQEMSKDLEEVKAK 120
Db      61 ALGKQLNLKLLDNWDSVTSTFSKLRQGLPVTQEFWDNLEKETEGLRQEMSKDLEEVKAK 120

QY      121 VQPYLDDFQKKWQEEEMELYRQKVEPLRAELOEGARQKHLHELQEKLSPLGEEMRDRARAHV 180
Db      121 VQPYLDDFQKKWQEEEMELYRQKVEPLRAELOEGARQKHLHELQEKLSPLGEEMRDRARAHV 180

QY      181 DALRTHLAPYSDELRLQRLAARLEALKENGARLAEYHAKATEHLSTLSEKAKPALEDLRQ 240
Db      181 DALRTHLAPYSDELRLQRLAARLEALKENGARLAEYHAKATEHLSTLSEKAKPALEDLRQ 240

QY      241 GLLPVLESFKVSFLSALSEYTKKLNQ 267
Db      241 GLLPVLESFKVSFLSALSEYTKKLNQ 267

RESULT 6
US-10-403-902A-30
; Sequence 30, Application US/10403902A
; Publication No. US20030224418A1
; GENERAL INFORMATION:
; APPLICANT: Braun, Andreas
; APPLICANT: Bansal, Aruna
; APPLICANT: Klyen, Patrick
; TITLE OF INVENTION: GENES AND POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISEASE AND THEIR USE
; FILE REFERENCE: 24736-2048B
; CURRENT APPLICATION NUMBER: US/10/403,902A
; CURRENT FILING DATE: 2003-07-21
; PRIOR APPLICATION NUMBER: 09/802,640
; PRIOR FILING DATE: 2001-03-09
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 267
; TYPE: PRT
; ORGANISM: Homo sapien
; US-10-403-902A-30

Query Match      100.0%; Score 1362; DB 4; Length 267;
Best Local Similarity 100.0%; Pred. No. 1e-92;
Matches 267; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MKAAVLTAVLFLTGSAQHFWQDEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGS 60
```

Db 1 MKA AVLTLAVLFTG SQARHFQQDEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFE GS 60

QY 61 ALGKQLNLKLLDNWDSVTSTFSKLRQLGPVTQEFWDNLEKETETGLRQEMSKDLEEVKAK 120

Db 61 ALGKQLNLKLLDNWDSVTSTFSKLRQLGPVTQEFWDNLEKETETGLRQEMSKDLEEVKAK 120

QY 121 VQPYLDDFQKKWQEEEMELYRQKVEPLRAELQEGARQKHLHQLKLSPLGEMRDRARAHV 180

Db 121 VQPYLDDFQKKWQEEEMELYRQKVEPLRAELQEGARQKHLHQLKLSPLGEMRDRARAHV 180

QY 181 DALRTHLAPYSDELQRRLAARLEALKENG GARLAEBYHAKATEHLSTLSEKAKPALEDLRQ 240

Db 181 DALRTHLAPYSDELQRRLAARLEALKENG GARLAEBYHAKATEHLSTLSEKAKPALEDLRQ 240

QY 241 GLLPVLESFKVSFLSAL EYTKKLN TQ 267

Db 241 GLLPVLESFKVSFLSAL EYTKKLN TQ 267

RESULT 7

US-10-186-288-10

; Sequence 10, Application US/10186288

; Publication No. US20040001810A1

; GENERAL INFORMATION:

; APPLICANT: Davis, Roger A.

; TITLE OF INVENTION: Compositions and Methods for Treating

; FILE REFERENCE: P-RD 5299

; CURRENT APPLICATION NUMBER: US/10/186,288

; PRIOR FILING DATE: 2002-06-26

; PRIOR APPLICATION NUMBER: US 09/893,366

; PRIOR FILING DATE: 2001-06-26

; NUMBER OF SEQ ID NOS: 13

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 10

; LENGTH: 267

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-186-288-10

Query Match 100.0%; Score 1362; DB 4; Length 267;

Best Local Similarity 100.0%; Pred. No. 1e-92;

Matches 267; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKA AVLTLAVLFTG SQARHFQQDEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFE GS 60

Db 1 MKA AVLTLAVLFTG SQARHFQQDEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFE GS 60

QY 61 ALGKQLNLKLLDNWDSVTSTFSKLRQLGPVTQEFWDNLEKETETGLRQEMSKDLEEVKAK 120

Db 61 ALGKQLNLKLLDNWDSVTSTFSKLRQLGPVTQEFWDNLEKETETGLRQEMSKDLEEVKAK 120

QY 121 VQPYLDDFQKKWQEEEMELYRQKVEPLRAELQEGARQKHLHQLKLSPLGEMRDRARAHV 180

Db 121 VQPYLDDFQKKWQEEEMELYRQKVEPLRAELQEGARQKHLHQLKLSPLGEMRDRARAHV 180

QY 181 DALRTHLAPYSDELQRRLAARLEALKENG GARLAEBYHAKATEHLSTLSEKAKPALEDLRQ 240

Db 181 DALRTHLAPYSDELQRRLAARLEALKENG GARLAEBYHAKATEHLSTLSEKAKPALEDLRQ 240

QY 241 GLLPVLESFKVSFLSAL EYTKKLN TQ 267

Db 241 GLLPVLESFKVSFLSAL EYTKKLN TQ 267

RESULT 8

US-10-038-854-219

; Sequence 219, Application US/10038854

; Publication No. US20040022781A1

; GENERAL INFORMATION:

; APPLICANT: Spytek, Kimberly A

; APPLICANT: Li, Li

; APPLICANT: Wolenc, Adam R

; APPLICANT: Vernet, Corine

; APPLICANT: Eisen, Andrew J

; APPLICANT: Liu, Xiaohong

; APPLICANT: Malyankar, Uriel M

; APPLICANT: Shimkets, Richard A

; APPLICANT: Tchernev, Velizar

; APPLICANT: Spaderna, Steven K

; APPLICANT: Gorman, Linda

; APPLICANT: Kekuda, Ramesh

; APPLICANT: Patturajan, Meera

; APPLICANT: Gusev, Vladimir Y

; APPLICANT: Gangolli, Esha A

; APPLICANT: Guo, Xiaojia S

; APPLICANT: Shenoy, Suresh G

; APPLICANT: Rastelli, Luca

; APPLICANT: Casman, Stacie J

; APPLICANT: Boldog, Ferenc

; APPLICANT: Burgess, Catherine E

; APPLICANT: Edinger, Shlomit R

; APPLICANT: Ellerman, Karen

; APPLICANT: Gunther, Erik

; APPLICANT: Smithson, Glennda

; APPLICANT: Millet, Isabelle

; APPLICANT: MacDougall, John R

; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same

; FILE REFERENCE: 21402-230

; CURRENT APPLICATION NUMBER: US/10/038,854

; CURRENT FILING DATE: 2003-01-22

; PRIOR APPLICATION NUMBER: 60/258,928

; PRIOR FILING DATE: 2000-12-29

; PRIOR APPLICATION NUMBER: 60/259,415

; PRIOR FILING DATE: 2001-01-02

; PRIOR APPLICATION NUMBER: 60/259,785

; PRIOR FILING DATE: 2001-01-04

; PRIOR APPLICATION NUMBER: 60/269,814

; PRIOR FILING DATE: 2001-02-20

; PRIOR APPLICATION NUMBER: 60/279,832

; PRIOR FILING DATE: 2001-03-29

; PRIOR APPLICATION NUMBER: 60/279,833

; PRIOR FILING DATE: 2001-03-29

; PRIOR APPLICATION NUMBER: 60/279,863

; PRIOR FILING DATE: 2001-03-29

; PRIOR APPLICATION NUMBER: 60/283,889

; PRIOR FILING DATE: 2001-04-13

; PRIOR APPLICATION NUMBER: 60/284,447

; PRIOR FILING DATE: 2001-04-18

; PRIOR APPLICATION NUMBER: 60/286,683

; PRIOR FILING DATE: 2001-04-25

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 411

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 219

; LENGTH: 267

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-038-854-219

Query Match 100.0%; Score 1362; DB 4; Length 267;

Best Local Similarity 100.0%; Pred. No. 1e-92;

Matches 267; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKA AVLTLAVLFTG SQARHFQQDEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFE GS 60

Db 1 MKA AVLTLAVLFTG SQARHFQQDEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFE GS 60

QY 61 ALGKQLNLKLLDNWDSVTSTFSKLRQLGPVTQEFWDNLEKETETGLRQEMSKDLEEVKAK 120

Db 61 ALGKQLNLKLLDNWDSVTSTFSKLRQLGPVTQEFWDNLEKETETGLRQEMSKDLEEVKAK 120

QY 121 VQPYLDDFQKKWQEEEMELYRQKVEPLRAELQEGARQKHLHQLKLSPLGEMRDRARAHV 180

Db 121 VQPYLDDFQKKWQEEEMELYRQKVEPLRAELQEGARQKHLHQLKLSPLGEMRDRARAHV 180

QY 181 DALRTHLAPYSDELRLQRLAARLEALKENGCGARLAELYHAKATEHLSTLSEKAKPALEDLRQ 240  
Db 181 DALRTHLAPYSDELRLQRLAARLEALKENGCGARLAELYHAKATEHLSTLSEKAKPALEDLRQ 240  
QY 241 GLLPVLESFKVSFLSALEEYTKLNTQ 267  
Db 241 GLLPVLESFKVSFLSALEEYTKLNTQ 267

RESULT 9  
US-10-038-854-226  
; Sequence 226, Application US/10038854  
; Publication No. US20040022781A1  
; GENERAL INFORMATION:  
; APPLICANT: Spytex, Kimberly A  
; APPLICANT: Li, Li  
; APPLICANT: Wolenc, Adam R  
; APPLICANT: Vernet, Corine  
; APPLICANT: Eisen, Andrew J  
; APPLICANT: Liu, Xiaochong  
; APPLICANT: Malyankar, Uriel M  
; APPLICANT: Shinkets, Richard A  
; APPLICANT: Tchernev, Velizar  
; APPLICANT: Spaderna, Steven K  
; APPLICANT: Gorman, Linda  
; APPLICANT: Kekuda, Ramesh  
; APPLICANT: Patturajan, Meera  
; APPLICANT: Gusev, Vladimir Y  
; APPLICANT: Gangolli, Esha A  
; APPLICANT: Guo, Xiaojia S  
; APPLICANT: Shenoy, Suresh G  
; APPLICANT: Rastelli, Luca  
; APPLICANT: Casman, Stacie J  
; APPLICANT: Boldog, Ferenc  
; APPLICANT: Burgess, Catherine E  
; APPLICANT: Edinger, Shlomit R  
; APPLICANT: Ellerman, Karen  
; APPLICANT: Gunther, Erik  
; APPLICANT: Smithson, Glennda  
; APPLICANT: Millet, Isabelle  
; APPLICANT: MacDougall, John R  
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same  
; FILE REFERENCE: 21402-230  
; CURRENT APPLICATION NUMBER: US/10/038,854  
; CURRENT FILING DATE: 2003-01-22  
; PRIOR APPLICATION NUMBER: 60/258,928  
; PRIOR FILING DATE: 2000-12-29  
; PRIOR APPLICATION NUMBER: 60/259,415  
; PRIOR FILING DATE: 2001-01-02  
; PRIOR APPLICATION NUMBER: 60/259,785  
; PRIOR FILING DATE: 2001-01-04  
; PRIOR APPLICATION NUMBER: 60/269,814  
; PRIOR FILING DATE: 2001-02-20  
; PRIOR APPLICATION NUMBER: 60/279,832  
; PRIOR FILING DATE: 2001-03-29  
; PRIOR APPLICATION NUMBER: 60/279,833  
; PRIOR FILING DATE: 2001-03-29  
; PRIOR APPLICATION NUMBER: 60/279,863  
; PRIOR FILING DATE: 2001-03-29  
; PRIOR APPLICATION NUMBER: 60/283,889  
; PRIOR FILING DATE: 2001-04-13  
; PRIOR APPLICATION NUMBER: 60/284,447  
; PRIOR FILING DATE: 2001-04-18  
; PRIOR APPLICATION NUMBER: 60/286,683  
; PRIOR FILING DATE: 2001-04-25  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 411  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 226  
; LENGTH: 267  
; TYPE: PRT  
; ORGANISM: Homo sapiens

US-10-038-854-226  
Query Match 100.0%; Score 1362; DB 4; Length 267;  
Best Local Similarity 100.0%; Pred. No. 1e-92;  
Matches 267; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MKA AVLTLAVLFTG SQARHFQQDEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGS 60  
Db 1 MKA AVLTLAVLFTG SQARHFQQDEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGS 60  
QY 61 ALGKQLNLKLLDNWDSVTSTFSKLREQLGPVTQEFWDNLEKETEGRLQEMSKDLEEVKAK 120  
Db 61 ALGKQLNLKLLDNWDSVTSTFSKLREQLGPVTQEFWDNLEKETEGRLQEMSKDLEEVKAK 120  
QY 121 VQPYLDDFQKKWQEEEMELYRQKVEPLRAELQEGARQKHLHELQEKLSPLGEEMRDRARAHV 180  
Db 121 VQPYLDDFQKKWQEEEMELYRQKVEPLRAELQEGARQKHLHELQEKLSPLGEEMRDRARAHV 180  
QY 181 DALRTHLAPYSDELRLQRLAARLEALKENGCGARLAELYHAKATEHLSTLSEKAKPALEDLRQ 240  
Db 181 DALRTHLAPYSDELRLQRLAARLEALKENGCGARLAELYHAKATEHLSTLSEKAKPALEDLRQ 240  
QY 241 GLLPVLESFKVSFLSALEEYTKLNTQ 267  
Db 241 GLLPVLESFKVSFLSALEEYTKLNTQ 267  
RESULT 10  
US-10-991-217-260  
; Sequence 260, Application US/10991217  
; Publication No. US20050148513A1  
; GENERAL INFORMATION:  
; APPLICANT: Dasseux, Jean-Louis  
; APPLICANT: Sekul, Renate  
; APPLICANT: Buttner, Klaus  
; APPLICANT: Cornut, Isabelle  
; APPLICANT: Metz, Gunther  
; APPLICANT: Dufourcq, Jean  
; TITLE OF INVENTION: GENE THERAPY APPROACHES TO  
; TITLE OF INVENTION: SUPPLY APOLIPOPROTEIN A-I AGONISTS AND THEIR  
; TITLE OF INVENTION: USE TO TREAT DYSLIPIDEMIC DISORDERS.  
; NUMBER OF SEQUENCES: 274  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds LLP  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: NY  
; COUNTRY: USA  
; ZIP: 10036-2811  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/991,217  
; FILING DATE: 16-NOV-2004  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/940,136  
; FILING DATE: 29-SEP-1997  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Coruzzi, Laura A  
; REGISTRATION NUMBER: 30,742  
; REFERENCE/DOCKET NUMBER: 009196-0007-999  
; TELEPHONE: 650-493-4935  
; TELEFAX: 650-493-5556  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 260:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 267 amino acids

```
;
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-10-991-217-260

Query Match      100.0%; Score 1362; DB 5; Length 267;
Best Local Similarity 100.0%; Pred. No. 1e-92;
Matches 267; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MKA AVLTLAVLFLTG SQARHFQQDEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGS 60
Db      1 MKA AVLTLAVLFLTG SQARHFQQDEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGS 60

QY      61 ALGKQLNLKLLDNWDSVTSTFSKLRQGLPVTQEFWDNLEKETEGLRQEMSKDLEEVKAK 120
Db      61 ALGKQLNLKLLDNWDSVTSTFSKLRQGLPVTQEFWDNLEKETEGLRQEMSKDLEEVKAK 120

QY      121 VQPYLDDFQKKWQEEEMELYRQKVEPLRAELQEGARQKLHELQEKLSPLGEEMRDRARAHV 180
Db      121 VQPYLDDFQKKWQEEEMELYRQKVEPLRAELQEGARQKLHELQEKLSPLGEEMRDRARAHV 180

QY      181 DALRTHLAPYSDELQRLLAARLEALKENG GARLA EYHAKATEHLSTLSEKAKPALEDLRQ 240
Db      181 DALRTHLAPYSDELQRLLAARLEALKENG GARLA EYHAKATEHLSTLSEKAKPALEDLRQ 240

QY      241 GLLPVLESFKVSFLSAL E EYTKKLNTQ 267
Db      241 GLLPVLESFKVSFLSAL E EYTKKLNTQ 267

RESULT 11
US-10-987-454-2
; Sequence 2, Application US/10987454
; Publication No. US20050172359A1
; GENERAL INFORMATION:
; APPLICANT: Reid, Alexandra
; APPLICANT: Moloney, Maurice
; TITLE OF INVENTION: METHODS FOR THE PRODUCTION OF APOLIPOPROTEINS IN TRANSGENIC
; TITLE OF INVENTION: PLANTS
; FILE REFERENCE: 9369-311
; CURRENT APPLICATION NUMBER: US/10/987,454
; PRIOR FILING DATE: 2004-11-15
; PRIOR APPLICATION NUMBER: US 60/519,606
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: US 60/579,733
; PRIOR FILING DATE: 2004-06-16
; NUMBER OF SEQ ID NOS: 251
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2
; LENGTH: 267
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-987-454-2

Query Match      100.0%; Score 1362; DB 5; Length 267;
Best Local Similarity 100.0%; Pred. No. 1e-92;
Matches 267; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MKA AVLTLAVLFLTG SQARHFQQDEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGS 60
Db      1 MKA AVLTLAVLFLTG SQARHFQQDEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGS 60

QY      61 ALGKQLNLKLLDNWDSVTSTFSKLRQGLPVTQEFWDNLEKETEGLRQEMSKDLEEVKAK 120
Db      61 ALGKQLNLKLLDNWDSVTSTFSKLRQGLPVTQEFWDNLEKETEGLRQEMSKDLEEVKAK 120

QY      121 VQPYLDDFQKKWQEEEMELYRQKVEPLRAELQEGARQKLHELQEKLSPLGEEMRDRARAHV 180
Db      121 VQPYLDDFQKKWQEEEMELYRQKVEPLRAELQEGARQKLHELQEKLSPLGEEMRDRARAHV 180

QY      181 DALRTHLAPYSDELQRLLAARLEALKENG GARLA EYHAKATEHLSTLSEKAKPALEDLRQ 240
```

```
Db      181 DALRTHLAPYSDELQRLLAARLEALKENG GARLA EYHAKATEHLSTLSEKAKPALEDLRQ 240

QY      241 GLLPVLESFKVSFLSAL E EYTKKLNTQ 267
Db      241 GLLPVLESFKVSFLSAL E EYTKKLNTQ 267

RESULT 12
US-11-017-037-15
; Sequence 15, Application US/11017037
; Publication No. US20050096277A1
; GENERAL INFORMATION:
; APPLICANT: GRAVERSEN, Jonas
; APPLICANT: MOESTRUP, Soren
; TITLE OF INVENTION: APOLIPOPROTEINS ANALOGUES
; FILE REFERENCE: GRAVERSEN1A
; CURRENT APPLICATION NUMBER: US/11/017,037
; CURRENT FILING DATE: 2004-12-21
; PRIOR APPLICATION NUMBER: US/09/987,107
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/264,022
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: DK PA2001 00057
; PRIOR FILING DATE: 2001-01-15
; PRIOR APPLICATION NUMBER: DK PA2000 01682
; PRIOR FILING DATE: 2000-11-10
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 267
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-017-037-15

Query Match      100.0%; Score 1362; DB 6; Length 267;
Best Local Similarity 100.0%; Pred. No. 1e-92;
Matches 267; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MKA AVLTLAVLFLTG SQARHFQQDEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGS 60
Db      1 MKA AVLTLAVLFLTG SQARHFQQDEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGS 60

QY      61 ALGKQLNLKLLDNWDSVTSTFSKLRQGLPVTQEFWDNLEKETEGLRQEMSKDLEEVKAK 120
Db      61 ALGKQLNLKLLDNWDSVTSTFSKLRQGLPVTQEFWDNLEKETEGLRQEMSKDLEEVKAK 120

QY      121 VQPYLDDFQKKWQEEEMELYRQKVEPLRAELQEGARQKLHELQEKLSPLGEEMRDRARAHV 180
Db      121 VQPYLDDFQKKWQEEEMELYRQKVEPLRAELQEGARQKLHELQEKLSPLGEEMRDRARAHV 180

QY      181 DALRTHLAPYSDELQRLLAARLEALKENG GARLA EYHAKATEHLSTLSEKAKPALEDLRQ 240
Db      181 DALRTHLAPYSDELQRLLAARLEALKENG GARLA EYHAKATEHLSTLSEKAKPALEDLRQ 240

QY      241 GLLPVLESFKVSFLSAL E EYTKKLNTQ 267
Db      241 GLLPVLESFKVSFLSAL E EYTKKLNTQ 267

RESULT 13
US-11-019-829-15
; Sequence 15, Application US/11019829
; Publication No. US20050136465A1
; GENERAL INFORMATION:
; APPLICANT: Hoffmann-La Roche Inc.
; TITLE OF INVENTION: Novel targets for obesity from subcutaneous fat
; FILE REFERENCE: 22304
; CURRENT APPLICATION NUMBER: US/11/019,829
; CURRENT FILING DATE: 2004-12-22
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 15
```



; LENGTH: 267  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: apolipoprotein A-I  
; LOCATION: (1)..(267)  
; OTHER INFORMATION: M27875.1  
US-11-019-829-15

Query Match 100.0%; Score 1362; DB 6; Length 267;  
Best Local Similarity 100.0%; Pred. No. 1e-92;  
Matches 267; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKAAVLTAVLFLTGSQARHFQQDEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGS 60  
Db 1 MKAAVLTAVLFLTGSQARHFQQDEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGS 60  
Qy 61 ALGKQLNLKLLDNWDSVTSTFSKLRQGLGPVTQEFWDNLEKETEGLRQEMSKDLEEVKAK 120  
Db 61 ALGKQLNLKLLDNWDSVTSTFSKLRQGLGPVTQEFWDNLEKETEGLRQEMSKDLEEVKAK 120  
Qy 121 VQPYLDDFQKKWQEEEMELYRQKVEPLRAELQEGARQKLHELQEKLSPLGEEMRDRARAHV 180  
Db 121 VQPYLDDFQKKWQEEEMELYRQKVEPLRAELQEGARQKLHELQEKLSPLGEEMRDRARAHV 180  
Qy 181 DALRTHLAPYSDELQRRLAARLEALKENGARLAEYHAKATEHLSTLSEKAKPALEDLRQ 240  
Db 181 DALRTHLAPYSDELQRRLAARLEALKENGARLAEYHAKATEHLSTLSEKAKPALEDLRQ 240  
Qy 241 GLLPVLESFKVSFLSALAEYTKKLNQ 267  
Db 241 GLLPVLESFKVSFLSALAEYTKKLNQ 267

RESULT 14  
US-11-017-059-15  
; Sequence 15, Application US/11017059  
; Publication No. US20050142639A1  
; GENERAL INFORMATION:  
; APPLICANT: GRAVERSEN, Jonas  
; APPLICANT: MOESTRUP, Soren  
; TITLE OF INVENTION: APOLIPOPROTEINS ANALOGUES  
; FILE REFERENCE: GRAVERSEN1A  
; CURRENT APPLICATION NUMBER: US/11/017,059  
; CURRENT FILING DATE: 2004-12-21  
; PRIOR APPLICATION NUMBER: US/09/987,107  
; PRIOR FILING DATE: 2001-11-13  
; PRIOR APPLICATION NUMBER: US 60/264,022  
; PRIOR FILING DATE: 2001-01-26  
; PRIOR APPLICATION NUMBER: DK PA2001 00057  
; PRIOR FILING DATE: 2001-01-15  
; PRIOR APPLICATION NUMBER: DK PA2000 01682  
; PRIOR FILING DATE: 2000-11-10  
; NUMBER OF SEQ ID NOS: 91  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 15  
; LENGTH: 267  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-017-059-15

Query Match 100.0%; Score 1362; DB 6; Length 267;  
Best Local Similarity 100.0%; Pred. No. 1e-92;  
Matches 267; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKAAVLTAVLFLTGSQARHFQQDEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGS 60  
Db 1 MKAAVLTAVLFLTGSQARHFQQDEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGS 60  
Qy 61 ALGKQLNLKLLDNWDSVTSTFSKLRQGLGPVTQEFWDNLEKETEGLRQEMSKDLEEVKAK 120  
Db 61 ALGKQLNLKLLDNWDSVTSTFSKLRQGLGPVTQEFWDNLEKETEGLRQEMSKDLEEVKAK 120

Qy 121 VQPYLDDFQKKWQEEEMELYRQKVEPLRAELQEGARQKLHELQEKLSPLGEEMRDRARAHV 180  
Db 121 VQPYLDDFQKKWQEEEMELYRQKVEPLRAELQEGARQKLHELQEKLSPLGEEMRDRARAHV 180  
Qy 181 DALRTHLAPYSDELQRRLAARLEALKENGARLAEYHAKATEHLSTLSEKAKPALEDLRQ 240  
Db 181 DALRTHLAPYSDELQRRLAARLEALKENGARLAEYHAKATEHLSTLSEKAKPALEDLRQ 240  
Qy 241 GLLPVLESFKVSFLSALAEYTKKLNQ 267  
Db 241 GLLPVLESFKVSFLSALAEYTKKLNQ 267

RESULT 15  
US-10-852-705A-4  
; Sequence 4, Application US/10852705A  
; Publication No. US20050191639A1  
; GENERAL INFORMATION:  
; APPLICANT: Vlaams Interuniversitair Instituut voor Biotechnol  
; TITLE OF INVENTION: Method to isolate genes involved in aging  
; FILE REFERENCE: RCO/FAC/V098  
; CURRENT APPLICATION NUMBER: US/10/852,705A  
; CURRENT FILING DATE: 2004-05-24  
; PRIOR APPLICATION NUMBER: EP01204600.9  
; PRIOR FILING DATE: 2001-11-29  
; NUMBER OF SEQ ID NOS: 55  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 4  
; LENGTH: 275  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: human APOA1 cDNA fragment  
US-10-852-705A-4

Query Match 100.0%; Score 1362; DB 5; Length 275;  
Best Local Similarity 100.0%; Pred. No. 1.1e-92;  
Matches 267; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKAAVLTAVLFLTGSQARHFQQDEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGS 60  
Db 9 MKAAVLTAVLFLTGSQARHFQQDEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGS 68  
Qy 61 ALGKQLNLKLLDNWDSVTSTFSKLRQGLGPVTQEFWDNLEKETEGLRQEMSKDLEEVKAK 120  
Db 69 ALGKQLNLKLLDNWDSVTSTFSKLRQGLGPVTQEFWDNLEKETEGLRQEMSKDLEEVKAK 128  
Qy 121 VQPYLDDFQKKWQEEEMELYRQKVEPLRAELQEGARQKLHELQEKLSPLGEEMRDRARAHV 180  
Db 129 VQPYLDDFQKKWQEEEMELYRQKVEPLRAELQEGARQKLHELQEKLSPLGEEMRDRARAHV 188  
Qy 181 DALRTHLAPYSDELQRRLAARLEALKENGARLAEYHAKATEHLSTLSEKAKPALEDLRQ 240  
Db 189 DALRTHLAPYSDELQRRLAARLEALKENGARLAEYHAKATEHLSTLSEKAKPALEDLRQ 248  
Qy 241 GLLPVLESFKVSFLSALAEYTKKLNQ 267  
Db 249 GLLPVLESFKVSFLSALAEYTKKLNQ 275

Search completed: March 28, 2006, 20:42:42  
Job time : 164 secs

***This Page Blank (uspto)***

GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 28, 2006, 20:27:48 ; Search time 47 Seconds  
(without alignments)  
469.668 Million cell updates/sec

Title: US-09-803-918A-2  
Perfect score: 1362  
Sequence: 1 MKA AVLTLAVLFLTGSQARH.....SPKVSFLSALBEYTKKLTNQ 267

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*  
1: /cgn2\_6/ptodata/1/iaa/5\_COMB.pep:\*  
2: /cgn2\_6/ptodata/1/iaa/6\_COMB.pep:\*  
3: /cgn2\_6/ptodata/1/iaa/H\_COMB.pep:\*  
4: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep:\*  
5: /cgn2\_6/ptodata/1/iaa/RE\_COMB.pep:\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1362	100.0	267	1 US-07-959-946-3	Sequence 3, Appli
2	1362	100.0	267	1 US-08-333-577-3	Sequence 3, Appli
3	1362	100.0	267	2 US-08-952-796-2	Sequence 2, Appli
4	1362	100.0	267	2 US-08-940-136-260	Sequence 260, App
5	1362	100.0	267	2 US-10-283-599-260	Sequence 260, App
6	1362	100.0	267	2 US-09-987-107-15	Sequence 15, Appli
7	1362	100.0	267	4 PCT-US92-08634-3	Sequence 3, Appli
8	1346	98.8	267	2 US-09-919-039-27	Sequence 27, Appli
9	1306	95.9	267	2 US-09-987-107-16	Sequence 16, Appli
10	1246.5	91.5	306	2 US-09-987-107-9	Sequence 9, Appli
11	1246	91.5	304	2 US-09-987-107-7	Sequence 7, Appli
12	1246	91.5	304	2 US-09-987-107-8	Sequence 8, Appli
13	1246	91.5	323	2 US-09-987-107-58	Sequence 58, Appli
14	1246	91.5	323	2 US-09-987-107-60	Sequence 60, Appli
15	1243.5	91.3	304	2 US-09-987-107-6	Sequence 6, Appli
16	1243.5	91.3	306	2 US-09-987-107-10	Sequence 10, Appli
17	1243.5	91.3	306	2 US-09-987-107-11	Sequence 11, Appli
18	1243.5	91.3	323	2 US-09-987-107-56	Sequence 56, Appli
19	1242.5	91.2	337	2 US-09-987-107-46	Sequence 46, Appli
20	1242	91.2	301	2 US-09-987-107-3	Sequence 3, Appli
21	1242	91.2	301	2 US-09-987-107-5	Sequence 5, Appli
22	1242	91.2	316	2 US-09-987-107-48	Sequence 48, Appli
23	1242	91.2	316	2 US-09-987-107-54	Sequence 54, Appli
24	1242	91.2	329	2 US-09-987-107-14	Sequence 14, Appli
25	1242	91.2	344	2 US-09-987-107-68	Sequence 68, Appli
26	1241	91.1	243	2 US-09-079-030-119	Sequence 119, App
27	1241	91.1	243	2 US-09-987-107-1	Sequence 1, Appli

28	1241	91.1	244	2 US-09-987-107-2	Sequence 2, Appli
29	1241	91.1	261	2 US-09-987-107-52	Sequence 52, Appli
30	1241	91.1	336	2 US-09-987-107-44	Sequence 44, Appli
31	1240.5	91.1	264	1 US-08-448-606-6	Sequence 6, Appli
32	1238	90.9	324	2 US-09-987-107-62	Sequence 62, Appli
33	1235	90.7	324	2 US-09-987-107-64	Sequence 64, Appli
34	1235	90.7	324	2 US-09-987-107-66	Sequence 66, Appli
35	1161.5	85.3	266	2 US-09-987-107-19	Sequence 19, Appli
36	1105	81.1	265	2 US-09-987-107-18	Sequence 18, Appli
37	1100.5	80.8	266	2 US-09-987-107-20	Sequence 20, Appli
38	1077	79.1	265	2 US-09-987-107-17	Sequence 17, Appli
39	1016	74.6	258	2 US-09-987-107-4	Sequence 4, Appli
40	1016	74.6	273	2 US-09-987-107-50	Sequence 50, Appli
41	1006	73.9	200	2 US-08-952-796-15	Sequence 15, Appli
42	975.5	71.6	265	2 US-09-987-107-21	Sequence 21, Appli
43	904.5	66.4	264	2 US-09-987-107-22	Sequence 22, Appli
44	842.5	61.9	259	2 US-09-987-107-23	Sequence 23, Appli
45	727.5	53.4	241	2 US-09-987-107-24	Sequence 24, Appli

ALIGNMENTS

RESULT 1  
US-07-959-946-3  
; Sequence 3, Application US/07959946  
; Patent No. 5408038  
; GENERAL INFORMATION:  
; APPLICANT: Smith, Richard K.  
; APPLICANT: Koduri, Raju  
; APPLICANT: Young, Stephen G.  
; APPLICANT: Witztum, Joseph L.  
; APPLICANT: Curtiss, Linda K.  
; TITLE OF INVENTION: Lipoprotein Assays Using Antibodies to a  
; TITLE OF INVENTION: Pan Native Epitope and Recombinant Antigens  
; NUMBER OF SEQUENCES: 20  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Dressler, Goldsmith, Shore, Sutker &  
; ADDRESSEE: Milnamow, Ltd.  
; STREET: 180 No. 5408038th Stetson, Suite 4700  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60601  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/959,946  
; FILING DATE: 19921008  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/901,706  
; FILING DATE: 18-JUN-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Gamson, Edward P.  
; REGISTRATION NUMBER: 29,381  
; REFERENCE/DOCKET NUMBER:  
; TELEPHONE: (312)616-5400  
; TELEFAX: (312)616-5460  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 267 amino acids  
; TYPE: AMINO ACID  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-07-959-946-3

Query Match 100.0%; Score 1362; DB 1; Length 267;  
Best Local Similarity 100.0%; Pred. No. 8.6e-109;







```
;
; LENGTH: 267 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-10-283-599-260

Query Match      100.0%; Score 1362; DB 2; Length 267;
Best Local Similarity 100.0%; Pred. No. 8.6e-109;
Matches 267; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MKAAVLTTLAVLFLTGSQARHFQQDEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGS 60
Db      1 MKAAVLTTLAVLFLTGSQARHFQQDEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGS 60

QY      61 ALGKQLNLKLLDNWDSVTSTFSKLRQQLGPVTQEFWDNLEKETETGLRQEMSKDLEEVKAK 120
Db      61 ALGKQLNLKLLDNWDSVTSTFSKLRQQLGPVTQEFWDNLEKETETGLRQEMSKDLEEVKAK 120

QY      121 VQPYLDDFQKKWQEEEMELYRQKVEPLRAELOEGARQKLHELQEKLSPLGEEMRDRARAHV 180
Db      121 VQPYLDDFQKKWQEEEMELYRQKVEPLRAELOEGARQKLHELQEKLSPLGEEMRDRARAHV 180

QY      181 DALRTHLAPYSDELQRLLAARLEALKENGGARLAEYHAKATEHLSTLSEKAKPALEDLRQ 240
Db      181 DALRTHLAPYSDELQRLLAARLEALKENGGARLAEYHAKATEHLSTLSEKAKPALEDLRQ 240

QY      241 GLLPVLESFKVSFLSALAEYTKKLNTQ 267
Db      241 GLLPVLESFKVSFLSALAEYTKKLNTQ 267
```

```
RESULT 6
US-09-987-107-15
; Sequence 15, Application US/09987107
; Patent No. 6897039
; GENERAL INFORMATION:
; APPLICANT: GRAVERSEN, Jonas
; APPLICANT: MOESTRUP, Soren
; TITLE OF INVENTION: APOLIPOPROTEINS ANALOGUES
; FILE REFERENCE: GRAVERSENIA
; CURRENT APPLICATION NUMBER: US/09/987,107
; CURRENT FILING DATE: 2001-11-13
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: DK PA2001 00057
; PRIOR FILING DATE: 2001-01-15
; PRIOR APPLICATION NUMBER: DK PA2000 01682
; PRIOR FILING DATE: 2000-11-10
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 267
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-987-107-15
```

```
Query Match      100.0%; Score 1362; DB 2; Length 267;
Best Local Similarity 100.0%; Pred. No. 8.6e-109;
Matches 267; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MKAAVLTTLAVLFLTGSQARHFQQDEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGS 60
Db      1 MKAAVLTTLAVLFLTGSQARHFQQDEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGS 60

QY      61 ALGKQLNLKLLDNWDSVTSTFSKLRQQLGPVTQEFWDNLEKETETGLRQEMSKDLEEVKAK 120
Db      61 ALGKQLNLKLLDNWDSVTSTFSKLRQQLGPVTQEFWDNLEKETETGLRQEMSKDLEEVKAK 120

QY      121 VQPYLDDFQKKWQEEEMELYRQKVEPLRAELOEGARQKLHELQEKLSPLGEEMRDRARAHV 180
Db      121 VQPYLDDFQKKWQEEEMELYRQKVEPLRAELOEGARQKLHELQEKLSPLGEEMRDRARAHV 180
```

```
QY      181 DALRTHLAPYSDELQRLLAARLEALKENGGARLAEYHAKATEHLSTLSEKAKPALEDLRQ 240
Db      181 DALRTHLAPYSDELQRLLAARLEALKENGGARLAEYHAKATEHLSTLSEKAKPALEDLRQ 240

QY      241 GLLPVLESFKVSFLSALAEYTKKLNTQ 267
Db      241 GLLPVLESFKVSFLSALAEYTKKLNTQ 267
```

```
RESULT 7
PCT-US92-08634-3
; Sequence 3, Application PC/TUS9208634
; GENERAL INFORMATION:
; APPLICANT: Smith, Richard K.
; APPLICANT: Koduri, Raju
; APPLICANT: Young, Stephen G.
; APPLICANT: Witztum, Joseph L.
; APPLICANT: Curtiss, Linda K.
; TITLE OF INVENTION: Lipoprotein Assays Using Antibodies to a
; NUMBER OF INVENTION: Pan Native Epitope and Recombinant Antigens
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Goldsmith, Shore, Sutker &
; ADDRESSEE: Milnamow, Ltd.
; STREET: 180 North Stetson, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/08634
; FILING DATE: 19921009
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,706
; FILING DATE: 18-JUN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Gamson, Edward P.
; REGISTRATION NUMBER: 29,381
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312)616-5400
; TELEFAX: (312)616-5460
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 267 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US92-08634-3
```

```
Query Match      100.0%; Score 1362; DB 4; Length 267;
Best Local Similarity 100.0%; Pred. No. 8.6e-109;
Matches 267; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MKAAVLTTLAVLFLTGSQARHFQQDEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGS 60
Db      1 MKAAVLTTLAVLFLTGSQARHFQQDEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGS 60

QY      61 ALGKQLNLKLLDNWDSVTSTFSKLRQQLGPVTQEFWDNLEKETETGLRQEMSKDLEEVKAK 120
Db      61 ALGKQLNLKLLDNWDSVTSTFSKLRQQLGPVTQEFWDNLEKETETGLRQEMSKDLEEVKAK 120

QY      121 VQPYLDDFQKKWQEEEMELYRQKVEPLRAELOEGARQKLHELQEKLSPLGEEMRDRARAHV 180
Db      121 VQPYLDDFQKKWQEEEMELYRQKVEPLRAELOEGARQKLHELQEKLSPLGEEMRDRARAHV 180
```

[illegible]

RESULT 8  
 US-09-919-039-27  
 ; Sequence 27, Application US/09919039  
 ; Patent No. 6727066  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Kaser, Matthew R.  
 ; TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES  
 ; FILE REFERENCE: PA-0035 US  
 ; CURRENT APPLICATION NUMBER: US/09/919,039  
 ; CURRENT FILING DATE: 2002-09-09  
 ; PRIOR APPLICATION NUMBER: 60/222,113  
 ; PRIOR FILING DATE: 2000-07-28  
 ; NUMBER OF SEQ ID NOS: 401  
 ; SOFTWARE: PERL Program  
 ; SEQ ID NO 27  
 ; LENGTH: 267  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: misc feature  
 ; OTHER INFORMATION: Incyte ID No. 6727066 2516070CD1  
 US-09-919-039-27

Query Match	98.8%;	Score 1346;	DB 2;	Length 267;
Best Local Similarity	98.9%;	Pred. No. 2e-107;		
Matches 264;	Conservative	1;	Mismatches 2;	Indels 0;
Gaps	0;			

QY	1	MKAAVLTLAVFLTGSQARHFVQODEPPQSPWDRVKOLATVYVDVLKDSGRDYVSQFEGS	60
Db	1		60
QY	61	ALGKQLNLKLLDNWDSVTSTFSKLREQLGPVTQEFWDNLEKETEGLRQEMSKDLEEVKAK	120
Db	61		120
QY	121	VQPYLDDFQKKWQEEEMELYRQKVEPLRAELQEGARQKLHELQEKLSPLGEEMDRARAHV	180
Db	121		180
QY	181	DALRTHLAPYSDELQRRLAARLEALKKENGGARLAEYHAKATEHLSTLSEKAKPALEDLRQ	240
Db	181	:	240
QY	241	GLLPVLESFKVSFLSALAEYTKKLNTQ	267
Db	241		267

RESULT 9  
US-09-987-107-16  
; Sequence 16, Application US/09987107  
; Patent No. 6897039  
; GENERAL INFORMATION:  
; APPLICANT: GRAVERSEN, Jonas  
; APPLICANT: MOESTRUP, Soren  
; TITLE OF INVENTION: APOLIPOPROTEINS ANALOGUES  
; FILE REFERENCE: GRAVERSEN1A  
; CURRENT APPLICATION NUMBER: US/09/987,107  
; CURRENT FILING DATE: 2001-11-13  
; PRIOR APPLICATION NUMBER: US 60/264,022  
; PRIOR FILING DATE: 2001-01-26  
; PRIOR APPLICATION NUMBER: DK PA2001 00057  
; PRIOR FILING DATE: 2001-01-15  
; PRIOR APPLICATION NUMBER: DK PA2000 01682

```

; PRIOR FILING DATE: 2000-11-10
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 267
; TYPE: prt
; ORGANISM: Macaca fascicularis
US-09-987-107-16

```

Query Match	95.9%;	Score 1306;	DB 2;	Length 267;	
Best Local Similarity	95.1%;	Pred. No. 5.4e-104;			
Matches 254;	Conservative 6;	Mismatches 7;	Indels 0;	Gaps 0;	
Qy	1	MKAAVLTIAVLFLTGSQARHFQQDEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGS	60		
Db	1	MKATVLTIAVLFLTGSQARHFQQDEPPQSPWDRVKDLVTVYVEALKDSGKDYVSQFEGS	60		
Qy	61	ALGKQLNLKLLDNWDSVTSTFSKLREQLGPTQEFWDNLEKETEGLRQEMSKDLEEVKAK	120		
Db	61	ALGKQLNLKLLDNWDSVTSTVSKLREQLGPTQEFWDNLEKETEGLRQEMSKDLEEVKAK	120		
Qy	121	VQPYLDDFKKQWQEEEMELYRQKVEPLRAELQEGARQKLHELQEKLSPLGEEMRDRARAHV	180		
Db	121	VQPYLDDFKKQWQEEEMELYRQKVEPLRAELHEGTRQKLHELHEKLSPLGEEVRDRARAHV	180		
Qy	181	DALRTHLAPYSDELQRQRLAARLEALKENGCGARLAEYHAKATEHLSTLSEKAKPALEDLRQ	240		
Db	181	DALRTHLAPYSDELQRQRLAARLEALKENGCGARLAEYHAKASEHLSTLSEKAKPALEDLRQ	240		
Qy	241	GLLPVLESFKVSFLSALEYTKKLNQ	267		
Db	241	GLLPVLESFKVSFLSALEYTKKLSQ	267		

**RESULT 10**

```

US-09-987-107-9
; Sequence 9, Application US/09987107
; Patent No. 6897039
; GENERAL INFORMATION:
; APPLICANT: GRAVERSEN, Jonas
; APPLICANT: MOESTRUP, Soren
; TITLE OF INVENTION: APOLIPROTEINS ANALOGUES
; FILE REFERENCE: GRAVERSEN1A
; CURRENT APPLICATION NUMBER: US/09/987,107
; CURRENT FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/264,022
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: DK PA2001 00057
; PRIOR FILING DATE: 2001-01-15
; PRIOR APPLICATION NUMBER: DK PA2000 01682
; PRIOR FILING DATE: 2000-11-10
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 9
; LENGTH: 306
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(58)
; OTHER INFORMATION: Trimerisation module from
; NAME/KEY: misc feature
; LOCATION: (59)..(63)
; OTHER INFORMATION: Linker
; NAME/KEY: misc feature
; LOCATION: (64)..(306)
; OTHER INFORMATION: Mature Apo A1
US-09-987-107-9

```

Query Match 91.5%; Score 1246.5; DB 2; Length 306;  
Best Local Similarity 95.0%; Pred. NO. 8e-99;  
Matches 247; Conservative 3; Mismatches 7; Indels 3; Gaps 1;

Query Match 91.5%; Score 1246.5; DB 2; Length 306;

Best Local Similarity	95.0%;	Pred. NO. 8e-99;	
Matches 247;	Conservative	3; Mismatches	7; Indels
			3; Gaps





```
; Sequence 58, Application US/09987107
; Patent No. 6897039
; GENERAL INFORMATION:
; APPLICANT: GRAVERSEN, Jonas
; APPLICANT: MOESTRUP, Soren
; TITLE OF INVENTION: APOLIPOPROTEINS ANALOGUES
; FILE REFERENCE: GRAVERSEN1A
; CURRENT APPLICATION NUMBER: US/09/987,107
; CURRENT FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/264,022
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: DK PA2001 00057
; PRIOR FILING DATE: 2001-01-15
; PRIOR APPLICATION NUMBER: DK PA2000 01682
; PRIOR FILING DATE: 2000-11-10
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 58
; LENGTH: 323
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: pT7H6 Trip-A-Fn-Apo A1-final - AmpR plasmid
US-09-987-107-58

Query Match          91.5%; Score 1246; DB 2; Length 323;
Best Local Similarity 100.0%; Pred. No. 9.5e-99;
Matches 244; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 24 QDEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGSALGKQLNLKLLDNWDSVTSTFSK 83
      |||||||
Db 80 QDEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGSALGKQLNLKLLDNWDSVTSTFSK 139
      |||||||

Qy 84 LREQLGPVTQEFWDNLEKETEGRLQEMSKDLEEVKAKVQPYLDDFQKKWQEEEMELYRQKV 143
      |||||||
Db 140 LREQLGPVTQEFWDNLEKETEGRLQEMSKDLEEVKAKVQPYLDDFQKKWQEEEMELYRQKV 199
      |||||||

Qy 144 EPLRAELQEGARQKLHELQEKLSPLGEEMRDRARAHVDALRTHLAPYSDELRLQRLAARLE 203
      |||||||
Db 200 EPLRAELQEGARQKLHELQEKLSPLGEEMRDRARAHVDALRTHLAPYSDELRLQRLAARLE 259
      |||||||

Qy 204 ALKENGGAARLAHYHAKATEHLSTLSEKAKPALEDLRQGLLPVLESFKVSFLSALEYTKK 263
      |||||||
Db 260 ALKENGGAARLAHYHAKATEHLSTLSEKAKPALEDLRQGLLPVLESFKVSFLSALEYTKK 319
      |||||||

Qy 264 LNTQ 267
      ||||
Db 320 LNTQ 323

RESULT 15
US-09-987-107-6
; Sequence 60, Application US/09987107
; Patent No. 6897039
; GENERAL INFORMATION:
; APPLICANT: GRAVERSEN, Jonas
; APPLICANT: MOESTRUP, Soren
; TITLE OF INVENTION: APOLIPOPROTEINS ANALOGUES
; FILE REFERENCE: GRAVERSEN1A
; CURRENT APPLICATION NUMBER: US/09/987,107
; CURRENT FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/264,022
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: DK PA2001 00057
; PRIOR FILING DATE: 2001-01-15
; PRIOR APPLICATION NUMBER: DK PA2000 01682
; PRIOR FILING DATE: 2000-11-10
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 60
; LENGTH: 304
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(58)
; OTHER INFORMATION: Trimerisation module from tetranectin
; NAME/KEY: misc_feature
; LOCATION: (59)..(61)
; OTHER INFORMATION: Linker
; NAME/KEY: misc_feature
; LOCATION: (62)..(304)
; OTHER INFORMATION: Mature Apo A1
US-09-987-107-6

Query Match          91.3%; Score 1243.5; DB 2; Length 304;
Best Local Similarity 95.0%; Pred. No. 1.4e-98;
Matches 247; Conservative 1; Mismatches 7; Indels 5; Gaps 1;

Qy 8 LAVLFLTGSAARHFWQDEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGSALGKQLN 67
      | : | |
Db 50 LQTVSLKGSSG-----HDEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGSALGKQLN 104
      |||||||

Qy 68 LKLLDNWDSVTSTFSKLREQLPVTQEFWDNLEKETEGRLQEMSKDLEEVKAKVQPYLDD 127
```

Db	105	LKLLDNWDSVTSTFSLRQGLPVTQEFWDNLSEKETEGLRQEMSKDLEEVKAKVQPYLDD	164
QY	128	FQKKWQEEMELYRQKVEPLRAELOEGARQKLIHELOEKLSPGLGEEMDRAPAHVDALRTHL	187
Db	165	FQKKWQEEMELYRQKVEPLRAELOEGARQKLIHELOEKLSPGLGEEMDRAPAHVDALRTHL	224
QY	188	APYSDELQRORLAARLEALKENGGARLAEBYHAKATEHLSTLSEKAKPALEDLRQGLLPVLE	247
Db	225	APYSDELQRORLAARLEALKENGGARLAEBYHAKATEHLSTLSEKAKPALEDLRQGLLPVLE	284
QY	248	SFKVSFLSALEEYTKCLNTQ	267
Db	285	SFKVSFLSALEEYTKCLNTQ	304

Search completed: March 28, 2006, 20:29:10  
Job time : 47 secs

November 2005

Published\_Applications\_Nucleic\_Acid and Published\_Applications\_Amino\_Acid database searches now generate two sets of results each. The Published\_Applications databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Newly published applications will appear in the Published\_Applications\_New databases; older published applications make up the Published\_Applications\_Main databases.

Searches run against Nucleic\_Acid\_Published\_Applications produce two sets of results, with the extensions **.rnpbm** (Published\_Applications\_NA\_Main) and **.rnpbn** (Published\_Applications\_NA\_New). Searches run against Amino\_Acid\_Published\_Applications produce two sets of results, with the extensions **.rapbm** (Published\_Applications\_AA\_Main) and **.rapbn** (Published\_Applications\_AA\_New).

***This Page Blank (uspto)***



GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 28, 2006, 20:40:08 ; Search time 24 Seconds  
(without alignments)  
328.125 Million cell updates/sec

Title: US-09-803-918A-2  
Perfect score: 1362  
Sequence: 1 MKA AVLTLAVLFLTGSQARH.....SFKVSFLSALEYTKKLTNTQ 267

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 174695 seqs, 29494374 residues

Total number of hits satisfying chosen parameters: 174695

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA New:  
1: /SIDS5/ptodata/1/pubpaa/US08 NEW PUB.pep.\*  
2: /SIDS5/ptodata/1/pubpaa/US06 NEW PUB.pep.\*  
3: /SIDS5/ptodata/1/pubpaa/US07 NEW PUB.pep.\*  
4: /SIDS5/ptodata/1/pubpaa/PCT NEW PUB.pep.\*  
5: /SIDS5/ptodata/1/pubpaa/US09 NEW PUB.pep.\*  
6: /SIDS5/ptodata/1/pubpaa/US10 NEW PUB.pep.\*  
7: /SIDS5/ptodata/1/pubpaa/US11 NEW PUB.pep.\*  
8: /SIDS5/ptodata/1/pubpaa/US60 NEW PUB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1276	93.7	250	5	US-09-990-087-2
2	1262.5	92.7	301	7	US-11-116-319-2
3	1257.5	92.3	258	7	US-11-116-319-19
4	1257.5	92.3	258	7	US-11-116-319-23
5	1256.5	92.3	258	7	US-11-116-319-21
6	1255.5	92.2	258	7	US-11-116-319-22
7	1254.5	92.1	258	7	US-11-116-319-20
8	1241	91.1	243	7	US-11-006-119-18
9	1241	91.1	243	7	US-11-116-319-1
10	1241	91.1	243	7	US-11-189-438-2
11	1233	90.5	243	7	US-11-189-438-3
12	1233	90.5	243	7	US-11-189-438-4
13	1229	90.2	243	7	US-11-189-438-1
14	1024	75.2	414	5	US-09-990-087-17
15	1019	74.8	422	5	US-09-990-087-19
16	1014.5	74.5	212	5	US-09-990-087-6
17	1010	74.2	201	5	US-09-990-087-9
18	956.5	70.2	392	5	US-09-990-087-45
19	947	69.5	201	5	US-09-990-087-43
20	945	69.4	201	5	US-09-990-087-44
21	761.5	55.9	168	5	US-09-990-087-23
22	759.5	55.8	168	5	US-09-990-087-29
23	733	53.8	160	6	US-10-475-075-171
24	327	24.0	67	7	US-11-055-309A-17
25	318	23.3	65	6	US-10-475-075-457

26	274.5	20.2	396	6	US-10-995-561-1005	Sequence 1005, Ap
27	200	14.7	366	5	US-09-978-360A-421	Sequence 421, App
28	200	14.7	366	7	US-11-000-463-897	Sequence 897, App
29	200	14.7	400	7	US-11-000-463-425	Sequence 425, App
30	179.5	13.2	317	6	US-10-995-561-828	Sequence 828, App
31	179.5	13.2	317	7	US-11-055-309A-5	Sequence 5, Appli
32	174.5	12.8	317	7	US-11-186-284-6	Sequence 6, Appli
33	174.5	12.8	317	7	US-11-055-309A-4	Sequence 4, Appli
34	171.5	12.6	317	7	US-11-055-309A-6	Sequence 6, Appli
35	142	10.4	1404	6	US-10-878-556A-169	Sequence 169, App
36	140	10.3	936	7	US-11-072-512-2621	Sequence 2621, Ap
37	137.5	10.1	860	7	US-11-019-711-59	Sequence 59, Appl
38	137	10.1	276	7	US-11-000-463-239	Sequence 239, App
39	133	9.8	2228	6	US-10-511-096-2	Sequence 2, Appli
40	133	9.8	2230	6	US-10-511-096-4	Sequence 4, Appli
41	133	9.8	2250	6	US-10-511-096-6	Sequence 6, Appli
42	133	9.8	2252	6	US-10-511-096-8	Sequence 8, Appli
43	129.5	9.5	989	6	US-10-821-234-975	Sequence 975, App
44	128.5	9.4	1976	7	US-11-069-834-54	Sequence 54, Appl
45	127.5	9.4	629	7	US-11-072-512-3226	Sequence 3226, Ap

ALIGNMENTS

RESULT 1  
US-09-990-087-2  
; Sequence 2, Application US/09990087  
; Publication No. US20060057662A1  
; GENERAL INFORMATION:  
; APPLICANT: Sligar, Steven  
; APPLICANT: Bayburt, Timothy  
; TITLE OF INVENTION: Membrane Scaffold Proteins  
; FILE REFERENCE: 87-00  
; CURRENT APPLICATION NUMBER: US/09/990,087  
; CURRENT FILING DATE: 2001-11-20  
; PRIOR APPLICATION NUMBER: US 60/252,233  
; PRIOR FILING DATE: 2000-11-20  
; NUMBER OF SEQ ID NOS: 46  
; SOFTWARE: PatentIn ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 250  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-990-087-2

Query Match	93.7%	Score 1276;	DB 5;	Length 250;
Best Local Similarity	100.0%	Pred. No. 1.2e-79;		
Matches 248;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	20	HFQQDEPPQSPWDRVKDLATVYVDVLKDSGRDYSQFEGSALGKQLNLKLDNWDVS	79	
Db	3	HFQQDEPPQSPWDRVKDLATVYVDVLKDSGRDYSQFEGSALGKQLNLKLDNWDVS	62	
QY	80	TFSKLREQLGPTQEFWDNLEKETEGLRQENSKDLEEVKAKVQPYLDDFQKKQEE	139	
Db	63	TFSKLREQLGPTQEFWDNLEKETEGLRQENSKDLEEVKAKVQPYLDDFQKKQEE	122	
QY	140	RQKVEPLRAELQEGARQKLHELQEKLSPLGEMRDRARAHVDALRTHLAPYSDEL	199	
Db	123	RQKVEPLRAELQEGARQKLHELQEKLSPLGEMRDRARAHVDALRTHLAPYSDEL	182	
QY	200	ARLEALKENGARLAELYHAKATEHLSTLSEKAKPALEDLRQGLLPVLESFKVSFL	259	
Db	183	ARLEALKENGARLAELYHAKATEHLSTLSEKAKPALEDLRQGLLPVLESFKVSFL	242	
QY	260	YTKKLTNTQ 267		
Db	243	YTKKLTNTQ 250		
RESULT 2				
US-11-116-319-2				

; Sequence 2, Application US/11116319  
; Publication No. US20050287636A1  
; GENERAL INFORMATION:  
; APPLICANT: Korea Research Institutes of Bioscience and Biotechnology  
; TITLE OF INVENTION: Prophylactic and therapeutic agents containing point mutants of  
; TITLE OF INVENTION: proapolipoprotein A-I for anti-atherosclerosis and  
; TITLE OF INVENTION: anti-hyperlipidemia  
; FILE REFERENCE:  
; CURRENT APPLICATION NUMBER: US/11/116,319  
; CURRENT FILING DATE: 2005-04-28  
; NUMBER OF SEQ ID NOS: 23  
; SOFTWARE: Kopatentin 1.71  
; SEQ ID NO 2  
; LENGTH: 301  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-116-319-2

Query Match 92.7%; Score 1262.5; DB 7; Length 301;  
Best Local Similarity 97.3%; Pred. No. 1.2e-78;  
Matches 248; Conservative 0; Mismatches 0; Indels 7; Gaps 1;

QY 20 HFQQ-----DEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGSALGKQLNLKLLD 72  
Db 47 HFQQAPRPPTDEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGSALGKQLNLKLLD 106  
QY 73 NWDSVTSTFSKLRQGLGPVTQEFWDNLEKETEGLRQEMSKDLEEVKAKVQPYLDDFQKKW 132  
Db 107 NWDSVTSTFSKLRQGLGPVTQEFWDNLEKETEGLRQEMSKDLEEVKAKVQPYLDDFQKKW 166  
QY 133 QEEMELYRQKVEPLRAELQEGARQKLHELQEKLSPLGEEMRDRARAHVDALRTHLAPYS 192  
Db 167 QEEMELYRQKVEPLRAELQEGARQKLHELQEKLSPLGEEMRDRARAHVDALRTHLAPYS 226  
QY 193 ELRQRLAARLEALKENGARLAEYHAKATEHLSTLSEKAKPALEDLRQGLLPVLESFKVS 252  
Db 227 ELRQRLAARLEALKENGARLAEYHAKATEHLSTLSEKAKPALEDLRQGLLPVLESFKVS 286  
QY 253 FLSALEEYTKKLNQ 267  
Db 287 FLSALEEYTKKLNQ 301

RESULT 3  
US-11-116-319-19  
; Sequence 19, Application US/11116319  
; Publication No. US20050287636A1  
; GENERAL INFORMATION:  
; APPLICANT: Korea Research Institutes of Bioscience and Biotechnology  
; TITLE OF INVENTION: Prophylactic and therapeutic agents containing point mutants of  
; TITLE OF INVENTION: proapolipoprotein A-I for anti-atherosclerosis and  
; TITLE OF INVENTION: anti-hyperlipidemia  
; FILE REFERENCE:  
; CURRENT APPLICATION NUMBER: US/11/116,319  
; CURRENT FILING DATE: 2005-04-28  
; NUMBER OF SEQ ID NOS: 23  
; SOFTWARE: Kopatentin 1.71  
; SEQ ID NO 19  
; LENGTH: 258  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: proapoA-I-A154E  
US-11-116-319-19

Query Match 92.3%; Score 1257.5; DB 7; Length 258;  
Best Local Similarity 96.9%; Pred. No. 2.2e-78;  
Matches 247; Conservative 0; Mismatches 1; Indels 7; Gaps 1;

QY 20 HFQQ-----DEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGSALGKQLNLKLLD 72  
Db 4 HFQQAPRPPTDEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGSALGKQLNLKLLD 63

QY 73 NWDSVTSTFSKLRQGLGPVTQEFWDNLEKETEGLRQEMSKDLEEVKAKVQPYLDDFQKKW 132  
Db 64 NWDSVTSTFSKLRQGLGPVTQEFWDNLEKETEGLRQEMSKDLEEVKAKVQPYLDDFQKKW 123  
QY 133 QEEMELYRQKVEPLRAELQEGARQKLHELQEKLSPLGEEMRDRARAHVDALRTHLAPYS 192  
Db 124 QEEMELYRQKVEPLRAELQEGARQKLHELQEKLSPLGEEMRDRAREHVDALRTHLAPYS 183  
QY 193 ELRQRLAARLEALKENGARLAEYHAKATEHLSTLSEKAKPALEDLRQGLLPVLESFKVS 252  
Db 184 ELRQRLAARLEALKENGARLAEYHAKATEHLSTLSEKAKPALEDLRQGLLPVLESFKVS 243  
QY 253 FLSALEEYTKKLNQ 267  
Db 244 FLSALEEYTKKLNQ 258

RESULT 4  
US-11-116-319-23  
; Sequence 23, Application US/11116319  
; Publication No. US20050287636A1  
; GENERAL INFORMATION:  
; APPLICANT: Korea Research Institutes of Bioscience and Biotechnology  
; TITLE OF INVENTION: Prophylactic and therapeutic agents containing point mutants of  
; TITLE OF INVENTION: proapolipoprotein A-I for anti-atherosclerosis and  
; TITLE OF INVENTION: anti-hyperlipidemia  
; FILE REFERENCE:  
; CURRENT APPLICATION NUMBER: US/11/116,319  
; CURRENT FILING DATE: 2005-04-28  
; NUMBER OF SEQ ID NOS: 23  
; SOFTWARE: Kopatentin 1.71  
; SEQ ID NO 23  
; LENGTH: 258  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: proapoA-I-A158E  
US-11-116-319-23

Query Match 92.3%; Score 1257.5; DB 7; Length 258;  
Best Local Similarity 96.9%; Pred. No. 2.2e-78;  
Matches 247; Conservative 0; Mismatches 1; Indels 7; Gaps 1;

QY 20 HFQQ-----DEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGSALGKQLNLKLLD 72  
Db 4 HFQQAPRPPTDEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGSALGKQLNLKLLD 63  
QY 73 NWDSVTSTFSKLRQGLGPVTQEFWDNLEKETEGLRQEMSKDLEEVKAKVQPYLDDFQKKW 132  
Db 64 NWDSVTSTFSKLRQGLGPVTQEFWDNLEKETEGLRQEMSKDLEEVKAKVQPYLDDFQKKW 123  
QY 133 QEEMELYRQKVEPLRAELQEGARQKLHELQEKLSPLGEEMRDRARAHVDALRTHLAPYS 192  
Db 124 QEEMELYRQKVEPLRAELQEGARQKLHELQEKLSPLGEEMRDRARAHVDALRTHLAPYS 183  
QY 193 ELRQRLAARLEALKENGARLAEYHAKATEHLSTLSEKAKPALEDLRQGLLPVLESFKVS 252  
Db 184 ELRQRLAARLEALKENGARLAEYHAKATEHLSTLSEKAKPALEDLRQGLLPVLESFKVS 243  
QY 253 FLSALEEYTKKLNQ 267  
Db 244 FLSALEEYTKKLNQ 258

RESULT 5  
US-11-116-319-21  
; Sequence 21, Application US/11116319  
; Publication No. US20050287636A1  
; GENERAL INFORMATION:  
; APPLICANT: Korea Research Institutes of Bioscience and Biotechnology  
; TITLE OF INVENTION: Prophylactic and therapeutic agents containing point mutants of  
; TITLE OF INVENTION: proapolipoprotein A-I for anti-atherosclerosis and  
; TITLE OF INVENTION: anti-hyperlipidemia

```
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/11/116,319
; CURRENT FILING DATE: 2005-04-28
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: KopatentIn 1.71
; SEQ ID NO 21
; LENGTH: 258
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: proapoA-I-V156K
US-11-116-319-21

Query Match      92.3%; Score 1256.5; DB 7; Length 258;
Best Local Similarity 96.9%; Pred. No. 2.6e-78;
Matches 247; Conservative 0; Mismatches 1; Indels 7; Gaps 1;

QY 20 HFWQQ-----DEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGSALGKQLNLKLLD 72
Db 4 HFWQQA PRPPTPDEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGSALGKQLNLKLLD 63

QY 73 NWDSVTSTFSKLRQQLGPVTQEFWDNLEKETEGRLQEMSKDLEEVKAKVQPYLDDFQKKW 132
Db 64 NWDSVTSTFSKLRQQLGPVTQEFWDNLEKETEGRLQEMSKDLEEVKAKVQPYLDDFQKKW 123

QY 133 QEEMELYRQKVEPLRAELQEGARQKLHELQEKLSPLGEMRDRARAHVDALRTHLAPYS 192
Db 124 QEEMELYRQKVEPLRAELQEGARQKLHELQEKLSPLGEMRDRARAHVDALRTHLAPYS 183

QY 193 ELRQRLAARLEALKENGARLAELYHAKATEHLSTLSEKAKPALEDLRQGLLPVLESFKVS 252
Db 184 ELRQRLAARLEALKENGARLAELYHAKATEHLSTLSEKAKPALEDLRQGLLPVLESFKVS 243

QY 253 FLSALEEYTKKLNQ 267
Db 244 FLSALEEYTKKLNQ 258

Query Match      92.2%; Score 1255.5; DB 7; Length 258;
Best Local Similarity 96.9%; Pred. No. 3e-78;
Matches 247; Conservative 0; Mismatches 1; Indels 7; Gaps 1;

QY 20 HFWQQ-----DEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGSALGKQLNLKLLD 72
Db 4 HFWQQA PRPPTPDEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGSALGKQLNLKLLD 63

QY 73 NWDSVTSTFSKLRQQLGPVTQEFWDNLEKETEGRLQEMSKDLEEVKAKVQPYLDDFQKKW 132
Db 64 NWDSVTSTFSKLRQQLGPVTQEFWDNLEKETEGRLQEMSKDLEEVKAKVQPYLDDFQKKW 123

QY 133 QEEMELYRQKVEPLRAELQEGARQKLHELQEKLSPLGEMRDRARAHVDALRTHLAPYS 192
US-11-116-319-22

Query Match      92.1%; Score 1254.5; DB 7; Length 258;
Best Local Similarity 96.9%; Pred. No. 3.5e-78;
Matches 247; Conservative 0; Mismatches 1; Indels 7; Gaps 1;

QY 20 HFWQQ-----DEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGSALGKQLNLKLLD 72
Db 4 HFWQQA PRPPTPDEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGSALGKQLNLKLLD 63

QY 73 NWDSVTSTFSKLRQQLGPVTQEFWDNLEKETEGRLQEMSKDLEEVKAKVQPYLDDFQKKW 132
Db 64 NWDSVTSTFSKLRQQLGPVTQEFWDNLEKETEGRLQEMSKDLEEVKAKVQPYLDDFQKKW 123

QY 133 QEEMELYRQKVEPLRAELQEGARQKLHELQEKLSPLGEMRDRARAHVDALRTHLAPYS 192
Db 124 QEEMELYRQKVEPLRAELQEGARQKLHELQEKLSPLGEMRDRARAEVDALRTHLAPYS 183

QY 193 ELRQRLAARLEALKENGARLAELYHAKATEHLSTLSEKAKPALEDLRQGLLPVLESFKVS 252
Db 184 ELRQRLAARLEALKENGARLAELYHAKATEHLSTLSEKAKPALEDLRQGLLPVLESFKVS 243

QY 253 FLSALEEYTKKLNQ 267
Db 244 FLSALEEYTKKLNQ 258

Query Match      92.2%; Score 1255.5; DB 7; Length 258;
Best Local Similarity 96.9%; Pred. No. 3e-78;
Matches 247; Conservative 0; Mismatches 1; Indels 7; Gaps 1;

QY 20 HFWQQ-----DEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGSALGKQLNLKLLD 72
Db 4 HFWQQA PRPPTPDEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGSALGKQLNLKLLD 63

QY 73 NWDSVTSTFSKLRQQLGPVTQEFWDNLEKETEGRLQEMSKDLEEVKAKVQPYLDDFQKKW 132
Db 64 NWDSVTSTFSKLRQQLGPVTQEFWDNLEKETEGRLQEMSKDLEEVKAKVQPYLDDFQKKW 123

QY 133 QEEMELYRQKVEPLRAELQEGARQKLHELQEKLSPLGEMRDRARAHVDALRTHLAPYS 192
```

```
Db 124 QEEMELYRQKVEPLRAELQEGARQKLHELQEKLSPLGEMRDRARAHVDALRTHLAPYS 183
QY 193 ELRQRLAARLEALKENGARLAELYHAKATEHLSTLSEKAKPALEDLRQGLLPVLESFKVS 252
Db 184 ELRQRLAARLEALKENGARLAELYHAKATEHLSTLSEKAKPALEDLRQGLLPVLESFKVS 243
QY 253 FLSALEEYTKKLNQ 267
Db 244 FLSALEEYTKKLNQ 258

RESULT 7
US-11-116-319-20
; Sequence 20, Application US/11/116319
; Publication No. US20050287636A1
; GENERAL INFORMATION:
; APPLICANT: Korea Research Institutes of Bioscience and Biotechnology
; TITLE OF INVENTION: Prophylactic and therapeutic agents containing point mutants of
; TITLE OF INVENTION: proapolipoprotein A-I for anti-atherosclerosis and
; TITLE OF INVENTION: anti-hyperlipidemia
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/11/116,319
; CURRENT FILING DATE: 2005-04-28
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: KopatentIn 1.71
; SEQ ID NO 20
; LENGTH: 258
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: proapoA-I-H155E
US-11-116-319-20

Query Match      92.1%; Score 1254.5; DB 7; Length 258;
Best Local Similarity 96.9%; Pred. No. 3.5e-78;
Matches 247; Conservative 0; Mismatches 1; Indels 7; Gaps 1;

QY 20 HFWQQ-----DEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGSALGKQLNLKLLD 72
Db 4 HFWQQA PRPPTPDEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGSALGKQLNLKLLD 63

QY 73 NWDSVTSTFSKLRQQLGPVTQEFWDNLEKETEGRLQEMSKDLEEVKAKVQPYLDDFQKKW 132
Db 64 NWDSVTSTFSKLRQQLGPVTQEFWDNLEKETEGRLQEMSKDLEEVKAKVQPYLDDFQKKW 123

QY 133 QEEMELYRQKVEPLRAELQEGARQKLHELQEKLSPLGEMRDRARAHVDALRTHLAPYS 192
Db 124 QEEMELYRQKVEPLRAELQEGARQKLHELQEKLSPLGEMRDRARAEVDALRTHLAPYS 183

QY 193 ELRQRLAARLEALKENGARLAELYHAKATEHLSTLSEKAKPALEDLRQGLLPVLESFKVS 252
Db 184 ELRQRLAARLEALKENGARLAELYHAKATEHLSTLSEKAKPALEDLRQGLLPVLESFKVS 243

QY 253 FLSALEEYTKKLNQ 267
Db 244 FLSALEEYTKKLNQ 258

RESULT 8
US-11-006-119-18
; Sequence 18, Application US/11006119
; Publication No. US20050260691A1
; GENERAL INFORMATION:
; APPLICANT: Ndao, Momar
; APPLICANT: Ward, Brian
; APPLICANT: Caffrey, Rebecca
; APPLICANT: Spithill, Terry
; APPLICANT: Li, Hongshan
; APPLICANT: Podust, Vladimir
; APPLICANT: Perichon, Regis
; APPLICANT: CIPHERgen Biosystems, Inc.
; TITLE OF INVENTION: Serum Biomarkers for Chagas Disease
```





; PRIOR APPLICATION NUMBER: US 60/590,689  
; PRIOR FILING DATE: 2004-07-23  
; NUMBER OF SEQ ID NOS: 23  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 3  
; LENGTH: 243  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-189-438-3

Query Match 90.5%; Score 1233; DB 7; Length 243;  
Best Local Similarity 99.6%; Pred. No. 9.4e-77;  
Matches 242; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 25 DEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGSALGKQLNLKLLDNWDSVTSTFSKL 84  
|||||  
DB 1 DEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGSALGKQLNLKLLDNWDSVTSTFSKL 60  
  
QY 85 REQLGPVTQEFWDNLEKETEGRLQEMSKDLEEVKAKVQPYLDDFQKKWQEEEMELYRQKVE 144  
|||||  
DB 61 REQLGPVTQEFWDNLEKETEGRLQEMSKDLEEVKAKVQPYLDDFQKKWQEEEMELYRQKVE 120  
  
QY 145 PLRAELQEGARQKLHELQEKLSPLGEEMRDRARAHVDALRTHLAPYSDELRLQRLAARLEA 204  
|||||  
DB 121 PLRAELQEGARQKLHELQEKLSPLGEEMRDCARAHVDALRTHLAPYSDELRLQRLAARLEA 180  
  
QY 205 LKENGGARLAEYHAKATEHLSLSEKAKPALEDLRQGLLPVLESFKVSFLSALEEYTKKL 264  
|||||  
DB 181 LKENGGARLAEYHAKATEHLSLSEKAKPALEDLRQGLLPVLESFKVSFLSALEEYTKKL 240  
  
QY 265 NTQ 267  
|||  
DB 241 NTQ 243

RESULT 12  
US-11-189-438-4  
; Sequence 4, Application US/11189438  
; Publication No. US20060030525A1  
; GENERAL INFORMATION:  
; APPLICANT: Marshall, Shannon Alicia  
; APPLICANT: Moore, Gregory  
; TITLE OF INVENTION: APOLIPOPROTEIN A-I DERIVATIVES WITH ALTERED IMMUNOGENICITY  
; FILE REFERENCE: 186832/US/2  
; CURRENT APPLICATION NUMBER: US/11/189,438  
; CURRENT FILING DATE: 2005-07-25  
; PRIOR APPLICATION NUMBER: US 60/590,689  
; PRIOR FILING DATE: 2004-07-23  
; NUMBER OF SEQ ID NOS: 23  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 4  
; LENGTH: 243  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-189-438-4

Query Match 90.5%; Score 1233; DB 7; Length 243;  
Best Local Similarity 99.6%; Pred. No. 9.4e-77;  
Matches 242; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 25 DEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGSALGKQLNLKLLDNWDSVTSTFSKL 84  
|||||  
DB 1 DEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGSALGKQLNLKLLDNWDSVTSTFSKL 60  
  
QY 85 REQLGPVTQEFWDNLEKETEGRLQEMSKDLEEVKAKVQPYLDDFQKKWQEEEMELYRQKVE 144  
|||||  
DB 61 REQLGPVTQEFWDNLEKETEGRLQEMSKDLEEVKAKVQPYLDDFQKKWQEEEMELYRQKVE 120  
  
QY 145 PLRAELQEGARQKLHELQEKLSPLGEEMRDRARAHVDALRTHLAPYSDELRLQRLAARLEA 204  
|||||  
DB 121 PLRAELQEGARQKLHELQEKLSPLGEEMRDRARAHVDALRTHLAPYSDELRLQRLAARLEA 180  
  
QY 205 LKENGGARLAEYHAKATEHLSLSEKAKPALEDLRQGLLPVLESFKVSFLSALEEYTKKL 264  
|||||

Db 181 LKENGGARLAEYHAKATEHLSLSEKAKPALEDLRQGLLPVLESFKVSFLSALEEYTKKL 240  
  
QY 265 NTQ 267  
|||  
DB 241 NTQ 243  
  
RESULT 13  
US-11-189-438-1  
; Sequence 1, Application US/11189438  
; Publication No. US20060030525A1  
; GENERAL INFORMATION:  
; APPLICANT: Marshall, Shannon Alicia  
; APPLICANT: Moore, Gregory  
; TITLE OF INVENTION: APOLIPOPROTEIN A-I DERIVATIVES WITH ALTERED IMMUNOGENICITY  
; FILE REFERENCE: 186832/US/2  
; CURRENT APPLICATION NUMBER: US/11/189,438  
; CURRENT FILING DATE: 2005-07-25  
; PRIOR APPLICATION NUMBER: US 60/590,689  
; PRIOR FILING DATE: 2004-07-23  
; NUMBER OF SEQ ID NOS: 23  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 1  
; LENGTH: 243  
; TYPE: PRT  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: Synthetic  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (151)..(151)  
; OTHER INFORMATION: Xaa can be Arginine or Cysteine  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (173)..(173)  
; OTHER INFORMATION: Xaa can be Arginine or Cysteine  
US-11-189-438-1

Query Match 90.2%; Score 1229; DB 7; Length 243;  
Best Local Similarity 99.2%; Pred. No. 1.8e-76;  
Matches 241; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
QY 25 DEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGSALGKQLNLKLLDNWDSVTSTFSKL 84  
|||||  
DB 1 DEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGSALGKQLNLKLLDNWDSVTSTFSKL 60  
  
QY 85 REQLGPVTQEFWDNLEKETEGRLQEMSKDLEEVKAKVQPYLDDFQKKWQEEEMELYRQKVE 144  
|||||  
DB 61 REQLGPVTQEFWDNLEKETEGRLQEMSKDLEEVKAKVQPYLDDFQKKWQEEEMELYRQKVE 120  
  
QY 145 PLRAELQEGARQKLHELQEKLSPLGEEMRDRARAHVDALRTHLAPYSDELRLQRLAARLEA 204  
|||||  
DB 121 PLRAELQEGARQKLHELQEKLSPLGEEMRDXARAHVDALRTHLAPYSDELRLQRLAARLEA 180  
  
QY 205 LKENGGARLAEYHAKATEHLSLSEKAKPALEDLRQGLLPVLESFKVSFLSALEEYTKKL 264  
|||||  
DB 181 LKENGGARLAEYHAKATEHLSLSEKAKPALEDLRQGLLPVLESFKVSFLSALEEYTKKL 240  
  
QY 265 NTQ 267  
|||  
DB 241 NTQ 243

RESULT 14  
US-09-990-087-17  
; Sequence 17, Application US/09990087  
; Publication No. US20060057662A1  
; GENERAL INFORMATION:  
; APPLICANT: Sligar, Steven  
; APPLICANT: Bayburt, Timothy  
; TITLE OF INVENTION: Membrane Scaffold Proteins  
; FILE REFERENCE: 87-00

```

; CURRENT APPLICATION NUMBER: US/09/990,087
; CURRENT FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: US 60/252,233
; PRIOR FILING DATE: 2000-11-20
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
; LENGTH: 414
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-09-990-087-17

Query Match      75.2%; Score 1024; DB 5; Length 414;
Best Local Similarity 88.5%; Pred. No. 2.5e-62;
Matches 208; Conservative 6; Mismatches 19; Indels 2; Gaps 1;

QY 35 VKDLATVYVDVLKDSGRDYVSQFE--GSALGKQLNLKLLDNWDSVTSTFSKLRQLGPVT 92
Db 180 LEDLRQGLLPVLESFKVSFLSALEYTKLNTQGTILKLLDNWDSVTSTFSKLRQLGPVT 239

QY 93 QEFWDNLEKETETGLRQEMSKDLEEVKAKVQPYLDDFQKKWQEEEMELYRQKVEPLRAELQE 152
Db 240 QEFWDNLEKETETGLRQEMSKDLEEVKAKVQPYLDDFQKKWQEEEMELYRQKVEPLRAELQE 299

QY 153 GARQKLHELQEKLSPLGEEMRDRARAHVDALRTHLAPYSDELQRQLAARLEALKENGGAR 212
Db 300 GARQKLHELQEKLSPLGEEMRDRARAHVDALRTHLAPYSDELQRQLAARLEALKENGGAR 359

QY 213 LAEYHAKATEHLSTLSEKAKPALEDLRQGLLPVLESFKVSFLSALEYTKKLNQ 267
Db 360 LAEYHAKATEHLSTLSEKAKPALEDLRQGLLPVLESFKVSFLSALEYTKKLNQ 414

RESULT 15
US-09-990-087-19
; Sequence 19, Application US/09990087
; Publication No. US20060057662A1
; GENERAL INFORMATION:
; APPLICANT: Sligar, Steven
; APPLICANT: Bayburt, Timothy
; TITLE OF INVENTION: Membrane Scaffold Proteins
; FILE REFERENCE: 87-00
; CURRENT APPLICATION NUMBER: US/09/990,087
; CURRENT FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: US 60/252,233
; PRIOR FILING DATE: 2000-11-20
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
; LENGTH: 422
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-09-990-087-19

Query Match      74.8%; Score 1019; DB 5; Length 422;
Best Local Similarity 85.3%; Pred. No. 5.6e-62;
Matches 209; Conservative 7; Mismatches 15; Indels 14; Gaps 2;

QY 35 VKDLATVYVDVLKDSGRDYVSQFEGSALGQLN-----LKLLDNWDSVTSTFS 82
Db 180 LEDLRQGLLPVLESFKVSFLSALE--EYTKLNTQGTGGSGGGTLLKLLDNWDSVTSTFS 237

QY 83 KLRQLGPVTQEFWDNLEKETETGLRQEMSKOLEEVKAKVQPYLDDFQKKWQEEEMELYRQK 142
Db 238 KLRQLGPVTQEFWDNLEKETETGLRQEMSKOLEEVKAKVQPYLDDFQKKWQEEEMELYRQK 297

QY 143 VEPLRAELQEGARQKLHELQEKLSPLGEEMRDRARAHVDALRTHLAPYSDELQRQLAARL 202
```

```

Db 298 VEPLRAELQEGARQKLHELQEKLSPLGEEMRDRARAHVDALRTHLAPYSDELQRQLAARL 357
QY 203 EALKENGGARLAEYHAKATEHLSTLSEKAKPALEDLRQGLLPVLESFKVSFLSALEYTK 262
Db 358 EALKENGGARLAEYHAKATEHLSTLSEKAKPALEDLRQGLLPVLESFKVSFLSALEYTK 417
QY 263 KLNQ 267
Db 418 KLNQ 422
```

Search completed: March 28, 2006, 20:43:13  
Job time : 25 secs

## Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension .rup) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC searcher.

**When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.**

***This Page Blank (uspto)***



GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 28, 2006, 20:20:38 ; Search time 231 Seconds  
(without alignments)  
815.481 Million cell updates/sec

Title: US-09-803-918A-2  
Perfect score: 1362  
Sequence: 1 MKA AVLTLAVLFLTG SQARH.....SFKVSFLSALEYTKKLNTQ 267

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt\_05.80:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1362	100.0	267	1	APOA1_HUMAN
2	1362	100.0	267	2	Q6Q785_HUMAN
3	1306	95.9	267	1	APOA1_MACFA
4	1306	95.9	267	1	APOA1_PAPHA
5	1161.5	85.3	266	1	APOA1_CANFA
6	1105	81.1	265	1	APOA1_PIG
7	1100.5	80.8	266	1	APOA1_RABIT
8	1077	79.1	265	1	APOA1_BOVIN
9	1012.5	74.3	264	1	APOA1_MESAU
10	975.5	71.6	265	1	APOA1_TUPGB
11	962	70.6	191	2	Q8HZ96_9PRIM
12	962	70.6	191	2	Q8HZ97_PANTR
13	947	69.5	191	2	Q8HZ95_PONPY
14	905.5	66.5	264	2	Q8BPD5_MOUSE
15	904.5	66.4	264	1	APOA1_MOUSE
16	896	65.8	263	2	O08855_MOUSE
17	895	65.7	263	2	O09042_MOUSE
18	849.5	62.4	259	2	Q5EBB2_RAT
19	842.5	61.9	259	1	APOA1_RAT
20	836	61.4	258	2	O09054_RAT
21	834	61.2	258	2	O08877_RAT
22	823	60.4	191	2	Q8HZ94_SAGOE
23	727.5	53.4	241	2	Q9TS49_ERIEU
24	705.5	51.8	264	1	APOA1_ANAPL
25	688.5	50.6	264	1	APOA1_CHICK
26	663.5	48.7	264	1	APOA1_COTJA
27	616	45.2	198	2	Q58EV2_MOUSE
28	526	38.6	260	2	Q7ZYS5_XENLA
29	519	38.1	260	2	Q7SZA1_XENLA
30	512	37.6	261	2	Q6DDC5_XENTR
31	327	24.0	67	2	Q9Y355_HUMAN

32	320	23.5	79	2	Q6LD50_9MURI	Q6ld50 mus sp. apo
33	312.5	22.9	82	2	Q29248_PIG	Q29248 sus scrofa
34	306.5	22.5	367	2	Q6P7H6_XENLA	Q6p7h6 xenopus lae
35	306	22.5	369	2	Q5XHD2_XENLA	Q5xhd2 xenopus lae
36	303.5	22.3	250	2	Q6PBB8_XENLA	Q6pbb8 xenopus lae
37	301	22.1	369	2	Q640E4_XENLA	Q640e4 xenopus lae
38	298.5	21.9	263	2	Q98TG6_ANGJA	Q98tg6 anguilla ja
39	295	21.7	368	2	Q66IL6_XENTR	Q66il6 xenopus tro
40	291	21.4	429	1	APOA4_MACFA	P33621 macaca fasc
41	279	20.5	260	2	Q6DHE2_BRARE	Q6dhe2 brachydanio
42	279	20.5	268	2	Q567B9_BRARE	Q567b9 brachydanio
43	275	20.2	262	1	APOA1_BRARE	O42363 brachydanio
44	274.5	20.2	396	1	APOA4_HUMAN	P06727 homo sapien
45	274.5	20.2	396	2	Q6Q787_HUMAN	Q6q787 homo sapien

ALIGNMENTS

RESULT 1  
APOA1\_HUMAN  
ID APOA1\_HUMAN STANDARD; PRT; 267 AA.  
AC P02647; Q6LDN9;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 13-SEP-2005 (Rel. 48, Last annotation update)  
DE Apolipoprotein A-I precursor (Apo-AI) (ApoA-I) [Contains:  
DE Apolipoprotein A-I(1-242)].  
GN Name=APOA1;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=83220822; PubMed=6406984;  
RA Shoulders C.C., Kornblihtt A.R., Munro B.S., Baralle F.E.;  
RT "Gene structure of human apolipoprotein A1.";  
RL Nucleic Acids Res. 11:2827-2837(1983).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=83220772; PubMed=6304641;  
RA Cheung P., Chan L.;  
RT "Nucleotide sequence of cloned cDNA of human apolipoprotein A-I.";  
RL Nucleic Acids Res. 11:3703-3715(1983).  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=84016011; PubMed=6413973;  
RA Karathanasis S.K., Zannis V.I., Breslow J.L.;  
RT "Isolation and characterization of the human apolipoprotein A-I  
gene.";  
RL Proc. Natl. Acad. Sci. U.S.A. 80:6147-6151(1983).  
RN [4]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=85026665; PubMed=6207999;  
RA Seilhamer J.J., Protter A.A., Frossard P., Levy-Wilson B.;  
RT "Isolation and DNA sequence of full-length cDNA and of the entire gene  
for human apolipoprotein AI -- discovery of a new genetic polymorphism  
in the apo AI gene.";  
RL DNA 3:309-317(1984).  
RN [5]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=84221405; PubMed=6328445;  
RA Sharpe C.R., Sidoli A., Shelley C.S., Lucero M.A., Shoulders C.C.,  
Baralle F.E.;  
RT "Human apolipoproteins AI, AII, CII and CIII. cDNA sequences and mRNA  
abundance.";  
RL Nucleic Acids Res. 12:3917-3932(1984).  
RN [6]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=84119464; PubMed=6198645;  
RA Law S.W., Brewer H.B. Jr.;

RT "Nucleotide sequence and the encoded amino acids of human  
RT apolipoprotein A-I mRNA.";  
RN Proc. Natl. Acad. Sci. U.S.A. 81:66-70(1984).  
RL [7]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=86008382; PubMed=2995392;  
RA Law S.W., Brewer H.B. Jr.;  
RT "Tangier disease. The complete mRNA sequence encoding for preproapo-A-  
RT J.";  
RL J. Biol. Chem. 260:12810-12814(1985).  
RN [8]  
RP NUCLEOTIDE SEQUENCE (VARIANT TANGIER).  
RX MEDLINE=88196137; PubMed=3129297;  
RA Makrides S.C., Ruiz-Opazo N., Hayden M., Nussbaum A.L., Breslow J.L.,  
RA Zannis V.I.;  
RT "Sequence and expression of Tangier apoA-I gene.";  
RL Eur. J. Biochem. 173:465-471(1988).  
RN [9]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=89377481; PubMed=2673706;  
RA Moguilevsky N., Roobol C., Loriau R., Guillaume J.P., Jacobs P.,  
RA Cravador A., Herzog A., Brouwers L., Scarso A., Gilles P.,  
RA Holmquist L., Carlson L.A., Bollen A.;  
RT "Production of human recombinant proapolipoprotein A-I in Escherichia  
RT coli: purification and biochemical characterization.";  
RL DNA 8:429-436(1989).  
RN [10]  
RP NUCLEOTIDE SEQUENCE.  
RA Bollen A., Gobert J., Wuelfert E.;  
RT "Expression of human proapolipoprotein A-1.";  
RL Patent number EP0293357, 30-NOV-1988.  
RN [11]  
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].  
RC TISSUE=Skeletal muscle;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
RA Schnurch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [12]  
RP PROTEIN SEQUENCE OF 19-27.  
RX MEDLINE=83256553; PubMed=6409108;  
RA Brewer H.B. Jr., Fairwell T., Kay L., Meng M., Ronan R., Law S.,  
RA Light J.A.;  
RT "Human plasma proapoA-I: isolation and amino-terminal sequence.";  
RL Biochem. Biophys. Res. Commun. 113:626-632(1983).  
RN [13]  
RP PROTEIN SEQUENCE OF 25-267.  
RX MEDLINE=75133493; PubMed=164450;  
RA Baker H.N., Gotto A.M. Jr., Jackson R.L.;  
RT "The primary structure of human plasma high density apolipoprotein  
RT glutamine I (ApoA-I). II. The amino acid sequence and alignment of  
RT cyanogen bromide fragments IV, III, and I.";  
RL J. Biol. Chem. 250:2725-2738(1975).  
RN [14]  
RP PROTEIN SEQUENCE OF 25-267.  
RX MEDLINE=78123731; PubMed=204308;

RA Brewer H.B. Jr., Fairwell T., Larue A., Ronan R., Houser A.,  
RA Bronzert T.J.;  
RT "The amino acid sequence of human APOA-I, an apolipoprotein isolated  
RT from high density lipoproteins.";  
RL Biochem. Biophys. Res. Commun. 80:623-630(1978).  
RN [15]  
RP PROTEIN SEQUENCE OF 25-56.  
RX MEDLINE=88331387; PubMed=3047170;  
RA Yui Y., Aoyama T., Morishita H., Takahashi M., Takatsu Y., Kawai C.;  
RT "Serum prostacyclin stabilizing factor is identical to apolipoprotein  
RT A-I (Apo A-I). A novel function of Apo A-I.";  
RL J. Clin. Invest. 82:803-807(1988).  
RN [16]  
RP PROTEIN SEQUENCE OF 25-48.  
RX MEDLINE=89380318; PubMed=2506184;  
RA Manjunath P., Marcel Y.L., Uma J., Seidah N.G., Chretien M.,  
RA Chapdelaine A.;  
RT "Apolipoprotein A-I binds to a family of bovine seminal plasma  
RT proteins.";  
RL J. Biol. Chem. 264:16853-16857(1989).  
RN [17]  
RP PROTEIN SEQUENCE OF 25-43.  
RX MEDLINE=88070603; PubMed=3120314;  
RA Prioli R.P., Ordovas J.M., Rosenberg I., Schaeffer E.J.,  
RA Pereira M.E.A.;  
RT "Similarity of cruzin, an inhibitor of Trypanosoma cruzi  
RT neuraminidase, to high-density lipoprotein.";  
RL Science 238:1417-1419(1987).  
RN [18]  
RP PROTEIN SEQUENCE OF 25-42.  
RC TISSUE=Heart;  
RX MEDLINE=95203287; PubMed=7895732;  
RA Corbett J.M., Wheeler C.H., Baker C.S., Yacoub M.H., Dunn M.J.;  
RT "The human myocardial two-dimensional gel protein database: update  
RT 1994.";  
RL Electrophoresis 15:1459-1465(1994).  
RN [19]  
RP PROTEIN SEQUENCE OF 25-34.  
RC TISSUE=Platelet;  
RX MEDLINE=22608298; PubMed=12665801; DOI=10.1038/nbt810;  
RA Gevaert K., Goethals M., Martens L., Van Damme J., Staes A.,  
RA Thomas G.R., Vandekerckhove J.;  
RT "Exploring proteomes and analyzing protein processing by mass  
RT spectrometric identification of sorted N-terminal peptides.";  
RL Nat. Biotechnol. 21:566-569(2003).  
RN [20]  
RP NUCLEOTIDE SEQUENCE OF 118-267.  
RX MEDLINE=83091059; PubMed=6294659;  
RA Breslow J.L., Ross D., McPherson J., Williams H.W., Kurnit D.,  
RA Nussbaum A.L., Karathanasis S.K., Zannis V.I.;  
RT "Isolation and characterization of cDNA clones for human  
RT apolipoprotein A-I.";  
RL Proc. Natl. Acad. Sci. U.S.A. 79:6861-6865(1982).  
RN [21]  
RP PALMITOYLATION.  
RX MEDLINE=86140194; PubMed=3005308;  
RA Hoeg J.M., Meng M.S., Ronan R., Fairwell T., Brewer H.B. Jr.;  
RT "Human apolipoprotein A-I. Post-translational modification by fatty  
RT acid acylation.";  
RL J. Biol. Chem. 261:3911-3914(1986).  
RN [22]  
RP PROCESSING.  
RX MEDLINE=83195100; PubMed=6405383;  
RA Zannis V.I., Karathanasis S.K., Keutmann H.T., Goldberger G.,  
RA Breslow J.L.;  
RT "Intracellular and extracellular processing of human apolipoprotein A-  
RT I: secreted apolipoprotein A-I isoprotein 2 is a propeptide.";  
RL Proc. Natl. Acad. Sci. U.S.A. 80:2574-2578(1983).  
RN [23]  
RP MASS SPECTROMETRY.  
RX MEDLINE=22503077; PubMed=12562854; DOI=10.1194/jlr.D200034-JLR200;  
RA Niederkofler E.E., Tubbs K.A., Kiernan U.A., Nedelkov D., Nelson R.W.;  
RT "Novel mass spectrometric immunoassays for the rapid structural



DR PIR; A26529; A26529.  
DR HSSP; P02647; 1GW4.  
DR SMR; P68292; 68-267.  
DR InterPro; IPR000074; ApoA1\_A4\_E.  
DR PANTHER; PTHR18976; ApoA1\_A4\_E; 1.  
DR Pfam; PF01442; Apolipoprotein; 1.  
KW Cholesterol metabolism; Direct protein sequencing; HDL;  
KW Lipid metabolism; Lipid transport; Plasma; Repeat; Signal;  
KW Steroid metabolism; Transport.  
FT SIGNAL 1 18  
FT PROPEP 19 24  
FT CHAIN 25 267  
FT REPEAT 68 89  
FT REPEAT 90 111  
FT REPEAT 112 122  
FT REPEAT 123 144  
FT REPEAT 145 166  
FT REPEAT 167 188  
FT REPEAT 189 210  
FT REPEAT 211 232  
FT REPEAT 233 243  
FT REPEAT 244 267  
FT REGION 68 267  
FT CONFLICT 13 13  
FT SEQUENCE 267 AA; 30735 MW; 869955C02408E21 CRC64;  
  
Query Match 95.9%; Score 1306; DB 1; Length 267;  
Best Local Similarity 95.1%; Pred. No. 9.9e-62;  
Matches 254; Conservative 6; Mismatches 7; Indels 0; Gaps 0;  
  
QY 1 MKA AVLTLAVLFLTG SQARHFQQDEPPQSPWDRVKDLATVYVDVKDSGRDYVSQFE GS 60  
Db 1 MKATVLT LAVLFLTG SQARHFQQDEPPQTPWDRVKDLVTVYVEALKDSGKYVSQFE GS 60  
  
QY 61 ALGKQLNLKLLDNWDSVTSTFSKLRQGLGPVTQEFWDNLEKETEGRLQEMSKDLEEVKAK 120  
Db 61 ALGKQLNLKLLDNWDSVTSTVSKLRQGLGPVTQEFWDNLEKETEGRLQEMSKDLEEVKAK 120  
  
QY 121 VQPYLDDFQKKWQEEEMELYRQKVEPLRAELQEGARQKLHELQEKLSPLGEMRDRARAHV 180  
Db 121 VQPYLDDFQKKWQEEEMELYRQKVEPLRAELHEGTRQKLHELHEKLSPLGEEVRDRARAHV 180  
  
QY 181 DALRTHLAPYSDELQRQLAARLEALKENGARLAAYHAKATEHLSTLSEKAKPALEDLRQ 240  
Db 181 DALRTHLAPYSDELQRQLAARLEALKENGARLAAYHAKASEHLSTLSEKAKPALEDLRQ 240  
  
QY 241 GLLPVLESFKVSFLSALEEYTKKLNTQ 267  
Db 241 GLLPVLESFKVSFLSALEEYTKKLSTQ 267  
  
RESULT 4  
APOA1\_PAPHA STANDARD; PRT; 267 AA.  
ID APOA1\_PAPHA STANDARD; PRT; 267 AA.  
AC P68293; P15568; P17929;  
DT 01-APR-1990 (Rel. 14, Created)  
DT 01-APR-1990 (Rel. 14, Last sequence update)  
DT 10-MAY-2005 (Rel. 47, Last annotation update)  
DE Apolipoprotein A-I precursor (Apo-AI) (ApoA-I).  
GN Name=APOA1;  
OS Papio hamadryas (Hamadryas baboon).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
OC Cercopithecidae; Cercopithecinae; Papio.  
OX NCBI\_TaxID=9557;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Liver;  
RX MEDLINE=89232739; PubMed=2907746; DOI=10.1016/0378-1119(88)90181-3;  
RA Hixson J.E., Borenstein S., Cox L.A., Rainwater D.L., Vandenberg J.L.;  
RT "The baboon gene for apolipoprotein A-I: characterization of a cDNA  
RT clone and identification of DNA polymorphisms for genetic studies of  
RT cholesterol metabolism.";

RL Gene 74:483-490(1988).  
CC -!- FUNCTION: Participates in the reverse transport of cholesterol  
CC from tissues to the liver for excretion by promoting cholesterol  
CC efflux from tissues and by acting as a cofactor for the lecithin  
CC cholesterol acyltransferase (LCAT).  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- TISSUE SPECIFICITY: Major protein of plasma HDL, also found in  
CC chylomicrons.  
CC -!- SIMILARITY: Belongs to the apolipoprotein A1/A4/E family.  
CC -----  
CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use as long as its content is in no way modified and this statement is not  
CC removed.  
CC -----  
CC EMBL; M35634; AAA35380.1; -; mRNA.  
DR HSSP; P02647; 1GW4.  
DR SMR; P68293; 68-267.  
DR InterPro; IPR000074; ApoA1\_A4\_E.  
DR PANTHER; PTHR18976; ApoA1\_A4\_E; 1.  
DR Pfam; PF01442; Apolipoprotein; 1.  
KW Cholesterol metabolism; HDL; Lipid metabolism; Lipid transport;  
KW Plasma; Repeat; Signal; Steroid metabolism; Transport.  
FT SIGNAL 1 18  
FT PROPEP 19 24  
FT CHAIN 25 267  
FT REPEAT 68 89  
FT REPEAT 90 111  
FT REPEAT 112 122  
FT REPEAT 123 144  
FT REPEAT 145 166  
FT REPEAT 167 188  
FT REPEAT 189 210  
FT REPEAT 211 232  
FT REPEAT 233 243  
FT REPEAT 244 267  
FT REGION 68 267  
FT SEQUENCE 267 AA; 30735 MW; 869955C02408E21 CRC64;  
  
Query Match 95.9%; Score 1306; DB 1; Length 267;  
Best Local Similarity 95.1%; Pred. No. 9.9e-62;  
Matches 254; Conservative 6; Mismatches 7; Indels 0; Gaps 0;  
  
QY 1 MKA AVLTLAVLFLTG SQARHFQQDEPPQSPWDRVKDLATVYVDVKDSGRDYVSQFE GS 60  
Db 1 MKATVLT LAVLFLTG SQARHFQQDEPPQTPWDRVKDLVTVYVEALKDSGKYVSQFE GS 60  
  
QY 61 ALGKQLNLKLLDNWDSVTSTFSKLRQGLGPVTQEFWDNLEKETEGRLQEMSKDLEEVKAK 120  
Db 61 ALGKQLNLKLLDNWDSVTSTVSKLRQGLGPVTQEFWDNLEKETEGRLQEMSKDLEEVKAK 120  
  
QY 121 VQPYLDDFQKKWQEEEMELYRQKVEPLRAELQEGARQKLHELQEKLSPLGEMRDRARAHV 180  
Db 121 VQPYLDDFQKKWQEEEMELYRQKVEPLRAELHEGTRQKLHELHEKLSPLGEEVRDRARAHV 180  
  
QY 181 DALRTHLAPYSDELQRQLAARLEALKENGARLAAYHAKATEHLSTLSEKAKPALEDLRQ 240  
Db 181 DALRTHLAPYSDELQRQLAARLEALKENGARLAAYHAKASEHLSTLSEKAKPALEDLRQ 240  
  
QY 241 GLLPVLESFKVSFLSALEEYTKKLNTQ 267  
Db 241 GLLPVLESFKVSFLSALEEYTKKLSTQ 267  
  
RESULT 5  
APOA1\_CANFA STANDARD; PRT; 266 AA.  
ID APOA1\_CANFA STANDARD; PRT; 266 AA.  
AC P02648;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 15-DEC-1998 (Rel. 37, Last sequence update)  
DT 10-MAY-2005 (Rel. 47, Last annotation update)  
DE Apolipoprotein A-I precursor (Apo-AI) (ApoA-I).



GN Name=APOA1;  
OS Canis familiaris (Dog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;  
OC Canis.  
OX NCBI\_TaxID=9615;  
RN [1]  
RP NUCLEOTIDE SEQUENCE [MRNA].  
RC TISSUE=Liver;  
RX MEDLINE=90132271; PubMed=2515239;  
RA Luo C.-C., Li W.-H., Chan L.;  
RT "Structure and expression of dog apolipoprotein A-I, E, and C-I mRNAs:  
RT implications for the evolution and functional constraints of  
RT apolipoprotein structure.";  
RL J. Lipid Res. 30:1735-1746(1989).  
RN [2]  
RP PROTEIN SEQUENCE OF 25-266.  
RX MEDLINE=82142425; PubMed=6801039;  
RA Chung H., Randolph A., Reardon I., Heinrikson R.L.;  
RT "The covalent structure of apolipoprotein A-I from canine high density  
RT lipoproteins.";  
RL J. Biol. Chem. 257:2961-2967(1982).  
RN [3]  
RP PROTEIN SEQUENCE OF 25-57 AND 262-265.  
RX MEDLINE=76210910; PubMed=179887; DOI=10.1016/0014-5793(76)80338-9;  
RA Nakai T., Whayne T.F., Tang J.;  
RT "The amino- and carboxyl-terminal sequences of canine apolipoprotein  
RT A-i.";  
RL FEBS Lett. 64:409-411(1976).  
RN [4]  
RP PROTEIN SEQUENCE OF 25-37.  
RC TISSUE=Heart;  
RX MEDLINE=98163340; PubMed=9504812;  
RA Dunn M.J., Corbett J.M., Wheeler C.H.;  
RT "HSC-2DPAGE and the two-dimensional gel electrophoresis database of  
RT dog heart proteins.";  
RL Electrophoresis 18:2795-2802(1997).  
CC -!- FUNCTION: Participates in the reverse transport of cholesterol  
CC from tissues to the liver for excretion by promoting cholesterol  
CC efflux from tissues and by acting as a cofactor for the lecithin  
CC cholesterol acyltransferase (LCAT).  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- TISSUE SPECIFICITY: Major protein of plasma HDL, also found in  
CC chylomicrons. Synthesized in the liver and small intestine.  
CC -!- SIMILARITY: Belongs to the apolipoprotein A1/A4/E family.  
CC -----  
CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use as long as its content is in no way modified and this statement is not  
CC removed.  
CC -----  
DR PIR; A60940; LPDGA1.  
DR HSSP; P02647; LAV1.  
DR SMR; P02648; 67-266.  
DR HSC-2DPAGE; P02648; DOG.  
DR Ensembl; ENSCAFG00000013320; Canis familiaris.  
DR InterPro; IPR000074; ApoA1\_A4\_E.  
DR PANTHER; PTHR18976; ApoA1\_A4\_E; 1.  
DR Pfam; PF01442; Apolipoprotein; 1.  
KW Cholesterol metabolism; Direct protein sequencing; HDL;  
KW Lipid metabolism; Lipid transport; Plasma; Repeat; Signal;  
KW Steroid metabolism; Transport.  
FT SIGNAL 1 18 By similarity.  
FT PROPEP 19 24  
FT CHAIN 25 266 Apolipoprotein A-I.  
FT REPEAT 67 88 1.  
FT REPEAT 89 110 2.  
FT REPEAT 111 121 3 (half-length).  
FT REPEAT 122 143 4.  
FT REPEAT 144 165 5.  
FT REPEAT 166 187 6.  
FT REPEAT 188 209 7.

FT REPEAT 210 231 8.  
FT REPEAT 232 242 9 (half-length).  
FT REPEAT 243 266 10.  
FT REGION 67 266 10 X approximate tandem repeats.  
FT CONFLICT 168 168 A -> G (in Ref. 2).  
FT CONFLICT 202 202 E -> Q (in Ref. 2).  
FT CONFLICT 235 235 E -> Q (in Ref. 2).  
FT CONFLICT 264 266 NAQ -> A (in Ref. 3).  
SQ SEQUENCE 266 AA; 30196 MW; A3202620C28A869D CRC64;  
  
Query Match 85.3%; Score 1161.5; DB 1; Length 266;  
Best Local Similarity 85.0%; Pred. No. 4.4e-54;  
Matches 227; Conservative 19; Mismatches 20; Indels 1; Gaps 1;  
  
QY 1 MKAAVLTAVLFLTGSQARHFQQDEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEQS 60  
Db 1 MKAALLTAVLFLTGSQARHFQQDE-PQSPWDRVKDLATVYVDVAVKDSGRDYVAQFEAS 59  
  
QY 61 ALGKQLNLKLLDNWDSVTSTFSKLRQQLRGVTVQEFWDNLEKETEGLRQEMSKDLEEVKAK 120  
Db 60 ALGKQLNLKLLDNWDSLSSTVTYKLRQIGPVTVQEFWDNLEKETEVLRQEMSKDLEEVKQK 119  
  
QY 121 VQPYLDDFQKKWQEMELYRQKVEPLRAELQEGARQKLHELQEKLSPLGEEPMRDARAHV 180  
Db 120 VQPYLDDFQKKWQEEVELYRQKVAPLGSELREGARQKLQELQEKLSPLAEELRDARTHV 179  
  
QY 181 DALRTHLAPYSDELQRLLAARLEALKENGARLAAYHAKATEHLSTLSEKAKPALEDLRQ 240  
Db 180 DALRAQLAPYSDDLRLRLAARLEALKEGGASLAAYHARASEQLSALGKARPALEDLRQ 239  
  
QY 241 GLLPVLESFKVSFLSALBEYTKLNTQ 267  
Db 240 GLLPVLESFKVSLLAIDEATKKLNAQ 266  
  
RESULT 6  
APOA1\_PIG STANDARD; PRT; 265 AA.  
AC P18648;  
DT 01-NOV-1990 (Rel. 16, Created)  
DT 01-FEB-1994 (Rel. 28, Last sequence update)  
DT 13-SEP-2005 (Rel. 48, Last annotation update)  
DE Apolipoprotein A-I precursor (Apo-AI) (ApoA-I).  
GN Name=APOA1;  
OS Sus scrofa (Pig).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;  
OC Sus.  
OX NCBI\_TaxID=9823;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=93224154; PubMed=8468059;  
RA Birchbauer A., Knipping G., Juritsch B., Aschauer H., Zechner R.;  
RT "Characterization of the apolipoprotein AI and CIII genes in the  
RT domestic pig.";  
RL Genomics 15:643-652(1993).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Brain, and Liver;  
RX MEDLINE=94125128; PubMed=8294940;  
RA Moeckel B., Zinke H., Flach R., Weiss B., Weiler-Guettler H.,  
RA Gassen H.;  
RT "Expression of apolipoprotein A-I in porcine brain endothelium in  
RT vitro.";  
RL J. Neurochem. 62:788-798(1994).  
RN [3]  
RP NUCLEOTIDE SEQUENCE OF 34-265.  
RC TISSUE=Brain;  
RX MEDLINE=90132667; PubMed=2105375;  
RA Weiler-Guettler H., Sommerfeldt M., Papandrikopoulou A., Mischek U.,  
RA Bonitz D., Frey A., Grupe M., Scheerer J., Gassen H.G.;  
RT "Synthesis of apolipoprotein A-1 in pig brain microvascular  
RT endothelial cells.";

J. Neurochem. 54:444-450(1990).  
[4]  
NUCLEOTIDE SEQUENCE OF 105-265, AND TISSUE SPECIFICITY.  
TISSUE=Liver;  
RX MEDLINE=93154581; PubMed=8428656; DOI=10.1016/0378-1119(93)90121-I;  
RA Trieu V.N., Hasler-Rapacz J., Rapacz J., Black D.D.;  
RT "Sequences and expression of the porcine apolipoprotein A-I and C-III  
mRNAs";  
RL Gene 123:173-179(1993).  
[5]  
NUCLEOTIDE SEQUENCE OF 105-265.  
RX MEDLINE=94085789; PubMed=7916724; DOI=10.1016/0378-1119(93)90105-C;  
RA Trieu V.N., Patel B., Zhan R., Black D.D.;  
RT "Sequence of the porcine apoA-I gene";  
RL Gene 134:267-270(1993).  
[6]  
PROTEIN SEQUENCE OF 25-265.  
RA Hasler-Rapacz J.O., Chaudhary R., Chowdhary B.P., Trieu V.N.,  
RA Jackson K., Gustavsson I., Rapacz J.;  
RL Submitted (OCT-1995) to Swiss-Prot.  
[7]  
PROTEIN SEQUENCE OF 25-34.  
RX MEDLINE=76184721; PubMed=178359;  
RA Mahley R.W., Weisgraber K.H., Innerarity T., Brewer H.B. Jr.;  
RT "Characterization of the plasma lipoproteins and apoproteins of the  
Erythrocebus patas monkey";  
RL Biochemistry 15:1928-1933(1976).  
CC -!- FUNCTION: Participates in the reverse transport of cholesterol  
from tissues to the liver for excretion by promoting cholesterol  
efflux from tissues and by acting as a cofactor for the lecithin  
cholesterol acyltransferase (LCAT).  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- TISSUE SPECIFICITY: Major protein of plasma HDL, also found in  
chylomicrons. Synthesized predominantly in the intestine and the  
liver.  
CC -!- DEVELOPMENTAL STAGE: Liver apoA-I expressed in fetal, newborn and  
suckling animals. Intestinal apoA-I only expressed in postpartum  
animals.  
CC -!- SIMILARITY: Belongs to the apolipoprotein A1/A4/E family.  
-----  
This Swiss-Prot entry is copyright. It is produced through a collaboration  
between the Swiss Institute of Bioinformatics and the EMBL outstation -  
the European Bioinformatics Institute. There are no restrictions on its  
use as long as its content is in no way modified and this statement is not  
removed.  
-----  
EMBL; L00626; AAA30992.1; -; Genomic\_DNA.  
DR EMBL; X69477; CAA49234.1; -; mRNA.  
DR EMBL; X17057; -; NOT ANNOTATED CDS; mRNA.  
DR EMBL; X59414; CAA42050.1; -; mRNA.  
DR PIR; A46018; A46018.  
DR PIR; JT0672; JT0672.  
DR PIR; S21830; S21830.  
DR PIR; S31394; S31394.  
DR HSSP; P02647; 1AV1.  
DR SMR; P18648; 67-265.  
DR InterPro; IPR000074; ApoA1\_A4\_E.  
DR PANTHER; PTHR18976; ApoA1\_A4\_E; 1.  
DR Pfam; PF01442; Apolipoprotein; 1.  
KW Cholesterol metabolism; Direct protein sequencing; HDL;  
KW Lipid metabolism; Lipid transport; Plasma; Repeat; Signal;  
KW Steroid metabolism; Transport.  
FT SIGNAL 1 18 By similarity.  
FT PROPEP 19 24  
FT CHAIN 25 265 Apolipoprotein A-I.  
FT REPEAT 67 88 1.  
FT REPEAT 89 110 2.  
FT REPEAT 111 121 3 (half-length).  
FT REPEAT 122 142 4.  
FT REPEAT 144 165 5.  
FT REPEAT 166 187 6.  
FT REPEAT 188 209 7.  
FT REPEAT 210 230 8.

FT REPEAT 231 241 9 (half-length).  
FT REPEAT 242 265 10.  
FT REGION 67 265 10 X approximate tandem repeats.  
FT CONFLICT 108 108 E -> K (in Ref. 3).  
FT CONFLICT 143 143 Missing (in Ref. 2 and 3).  
FT CONFLICT 173 173 D -> S (in Ref. 4).  
FT CONFLICT 180 180 E -> A (in Ref. 2 and 3).  
FT CONFLICT 185 186 HV -> QL (in Ref. 1 and 6).  
FT CONFLICT 209 209 G -> D (in Ref. 2 and 3).  
FT CONFLICT 224 224 A -> G (in Ref. 4).  
SQ SEQUENCE 265 AA; 30325 MW; 2C6E578318ECF69C CRC64;  
  
Query Match 81.1%; Score 1105; DB 1; Length 265;  
Best Local Similarity 80.9%; Pred. No. 4.3e-51;  
Matches 216; Conservative 20; Mismatches 29; Indels 2; Gaps 2;  
  
QY 1 MKAAVLTTLAVLTLTGSQARHFQWQDEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEQS 60  
Db 1 MKAAVLTTLAVLTLTGSQARHFQWQDD-PQSPWDRVKDFATVYVDALKDSGRDYVAQFEAS 59  
  
QY 61 ALGKQLNLKLLDNWDSVTSTFSKLRQLGVPVQEFWDNLEKETEGLRQEMSKDLEEVKAK 120  
Db 60 ALGKHLNLKLLDNWDSLSGSTFTKVRQLGVPVQEFWDNLEKETEGLRQEMSKDLEEVKKK 119  
  
QY 121 VQPYLDDFQKKWQEMELYRQKVEPLRAELQEGARQKLHELQEKLSPLGEEMRDRARAHV 180  
Db 120 VQPYLDDFQKKWQEMETYRQKMAPLGAEFREGARQKQVQLQEKLSPLAEELRDLRAHV 179  
  
QY 181 DALRTHLAPYSDELQRRLAARLEALKENGARLAELYHAKATEHLSTLSEKAKPALEDLRQ 240  
Db 180 EALRQHVAPYSDDLRLRQRMARFEALKEGGGS-LAEYQAKAQEQALKGEKAKPALEDLRQ 238  
  
QY 241 GLLPVLESFKVSFLSALBEYTKLNTQ 267  
Db 239 GLLPVLENLKVSIILAAIDEASKKLNAQ 265  
  
RESULT 7  
APOA1\_RABBIT STANDARD; PRT; 266 AA.  
AC P09809;  
DT 01-MAR-1989 (Rel. 10, Created)  
DT 01-JAN-1990 (Rel. 13, Last sequence update)  
DT 10-MAY-2005 (Rel. 47, Last annotation update)  
DE Apolipoprotein A-I precursor (Apo-AI) (ApoA-I).  
GN Name=APOA1;  
OS Oryctolagus cuniculus (Rabbit).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Lagomorpha; Leporidae;  
OC Oryctolagus.  
OX NCBI\_TaxID=9986;  
RN [1]\_TaxID=9986;  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=2ZAP AI; TISSUE=Small intestine;  
RA Paraskevopoulou T.B., Kritsis A., Zannis V.I.;  
RL Submitted (JUL-1989) to the EMBL/GenBank/DBJ databases.  
[2]  
RN NUCLEOTIDE SEQUENCE.  
RP TISSUE=Intestine;  
RX MEDLINE=88082866; PubMed=3121329;  
RA Pan T.C., Hao Q.L., Yamin T.T., Dai P.H., Chen B.S., Chen S.L.,  
RA Kroon P.A., Chao Y.S.;  
RT "Rabbit apolipoprotein A-I mRNA and gene. Evidence that rabbit  
apolipoprotein A-I is synthesized in the intestine but not in the  
liver.";  
RL Eur. J. Biochem. 170:99-104(1987).  
[3]  
RP PROTEIN SEQUENCE OF 25-266.  
RX MEDLINE=87030294; PubMed=3095115;  
RA Yang C., Yang T., Pownall H.J., Gatto A.M. Jr.;  
RT "The primary structure of apolipoprotein A-I from rabbit high-density  
lipoprotein.";  
RL Eur. J. Biochem. 160:427-431(1986).

-!- FUNCTION: Participates in the reverse transport of cholesterol from tissues to the liver for excretion by promoting cholesterol efflux from tissues and by acting as a cofactor for the lecithin cholesterol acyltransferase (LCAT).

-!- SUBCELLULAR LOCATION: Secreted.

-!- TISSUE SPECIFICITY: Major protein of plasma HDL, also found in chylomicrons.

-!- SIMILARITY: Belongs to the apolipoprotein A1/A4/E family.

-----

This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.

-----

EMBL; X15908; CAA34024.1; -; mRNA.

EMBL; X06658; CAA29857.1; -; mRNA.

EMBL; X06659; CAA29858.1; -; Genomic\_DNA.

PIR; S06064; LPRB12.

HSSP; P02647; 1AV1.

SMR; P09809; 67-266.

InterPro; IPR000074; ApoA1\_A4\_E.

PANTHER; PTHR18976; ApoA1\_A4\_E; 1.

Pfam; PF01442; Apolipoprotein\_1.

Cholesterol metabolism; Direct protein sequencing; HDL;

Lipid metabolism; Lipid transport; Plasma; Repeat; Signal;

Steroid metabolism; Transport.

SIGNAL 1 18

PROPEP 19 24

CHAIN 25 266

Apolipoprotein A-I.

1.

2.

3 (half-length).

4.

5.

6.

7.

8.

9 (half-length).

10.

10 X approximate tandem repeats.

A -> R (in Ref. 2; CAA29858).

Missing (in Ref. 3).

V -> I (in Ref. 2; CAA29858).

E -> Q (in Ref. 3).

Y -> F (in Ref. 2; CAA29857).

A -> V (in Ref. 2; CAA29858 and 3).

R -> G (in Ref. 2; CAA29858/CAA29857).

N -> Q (in Ref. 3).

Missing (in Ref. 2; CAA29858/CAA29857).

S -> K (in Ref. 2; CAA29858/CAA29857).

VL -> LV (in Ref. 3).

L -> V (in Ref. 2; CAA29858/CAA29857).

30591 MW; OFF6DB386497C7D2 CRC64;

266 AA; 30591 MW; OFF6DB386497C7D2 CRC64;

Query Match 80.8%; Score 1100.5; DB 1; Length 266;

Best Local Similarity 80.1%; Pred. No. 7.5e-51;

Matches 214; Conservative 25; Mismatches 27; Indels 1; Gaps 1;

1 MKAAVLTAVLFLTGSGARHFQQDEPPQSPWDRVKLATVYVDVLKDSGRDYVSQFEGS 60

1 MKAVVLTLAVLFLTGSGARHFQORDE-PRSSWDKIKDFATVYVDVTKDSGREYVAQFEAS 59

61 ALGKQLNLKLLDNWDSVTSFKLREQLGPVTQEFWDNLEKETEGLRQEMSKDLREVKAK 120

60 AFGKQLNLKLLDNWDSLSSTVSKLQELGPVTQEFWDNLEKETEGLRQEMSKDLQEVROK 119

121 VQPYLDDFQKKWQEEEMELYRQKVEPLRAELQEGARQKHLQELKSLPLGEEMRDRARHV 180

120 VQPYLDEFQKKWQEEVERYRQKVEPLGAELRESARQKLTQELQELKSLPLAEELRDSARTHV 179

181 DALRTHLAPYSDELRLQRLAARLEALKEKNGGARLAHYHAKATEHLSTLSEKAKPALEDLRQ 240

Db 180 DTLRTKLAPYSNELQORLAARLESIKEGGASLAASYQAKAREHLSVLSEKARPALEDLRQ 239

QY 241 GLLPVLSEFKVSFLSALSEYTKKLNTQ 267

Db 240 GLLPVLSEFKASVQNVLDKATKLTQ 266

-----

RESULT 8

APOA1\_BOVIN STANDARD; PRT; 265 AA.

AC P15497;

DT 01-APR-1990 (Rel. 14, Created)

DT 01-MAY-1992 (Rel. 22, Last sequence update)

DT 10-MAY-2005 (Rel. 47, Last annotation update)

DE Apolipoprotein A-I precursor (Apo-AI) (ApoA-I).

GN Name=ApoA1;

OS Bos taurus (Bovine).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;

OC Pecora; Bovidae; Bovinae; Bos.

OX NCBI\_TaxID=9913;

RN [1]

RP NUCLEOTIDE SEQUENCE [MRNA].

RX MEDLINE=90348478; PubMed=2117227;

RA O'Huigin C., Chan L., Li W.H.;

RT "Cloning and sequencing of bovine apolipoprotein A-I cDNA and molecular evolution of apolipoproteins A-I and B-100.";

RL Mol. Biol. Evol. 7:327-339(1990).

RN [2]

RP PROTEIN SEQUENCE OF 19-265.

RX MEDLINE=92153895; PubMed=1739745; DOI=10.1016/0005-2760(92)90104-4;

RA Sparrow D.A., Lee B.R., Laplaud M.P., Aubiron S., Bauchart D., Chapman J.M., Gotto A.M. Jr., Yang C.Y., Sparrow J.T.;

RT "Plasma lipid transport in the prerinant calf, Bos spp: primary structure of bovine apolipoprotein A-I.";

RL Biochim. Biophys. Acta 1123:145-150(1992).

RN [3]

RP PROTEIN SEQUENCE OF 25-70.

RX MEDLINE=90147795; PubMed=2105728;

RA Aubiron S., Sparrow D.A., Beaubatie L., Bauchart D., Sparrow J.T., Laplaud M.P., Chapman J.M.;

RT "Characterization and amino-terminal sequence of apolipoprotein A1 from plasma high density lipoproteins in the prerinant calf, Bos spp.";

RL Biochem. Biophys. Res. Commun. 166:833-839(1990).

CC -!- FUNCTION: Participates in the reverse transport of cholesterol from tissues to the liver for excretion by promoting cholesterol efflux from tissues and by acting as a cofactor for the lecithin cholesterol acyltransferase (LCAT).

CC -!- SUBCELLULAR LOCATION: Secreted.

CC -!- TISSUE SPECIFICITY: Major protein of plasma HDL, also found in chylomicrons.

CC -!- SIMILARITY: Belongs to the apolipoprotein A1/A4/E family.

-----

This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.

-----

EMBL; M35870; AAA30381.1; -; mRNA.

PIR; I45853; A56858.

HSSP; P02647; 1AV1.

SMR; P15497; 67-265.

InterPro; IPR000074; ApoA1\_A4\_E.

PANTHER; PTHR18976; ApoA1\_A4\_E; 1.

Pfam; PF01442; Apolipoprotein\_1.

Cholesterol metabolism; Direct protein sequencing; HDL;

Lipid metabolism; Lipid transport; Plasma; Repeat; Signal;

Steroid metabolism; Transport.

SIGNAL 1 18

PROPEP 19 24

CHAIN 25 265

Apolipoprotein A-I.

FT REPEAT 67 88 1.  
FT REPEAT 89 110 2.  
FT REPEAT 111 121 3 (half-length).  
FT REPEAT 122 143 4.  
FT REPEAT 144 165 5.  
FT REPEAT 166 187 6.  
FT REPEAT 188 209 7.  
FT REPEAT 210 230 8.  
FT REPEAT 231 241 9 (half-length).  
FT REPEAT 242 265 10.  
FT REGION 67 265 10 X approximate tandem repeats.  
FT CONFLICT 185 186 QL -> HV (in Ref. 2).  
SQ SEQUENCE 265 AA; 30276 MW; 06A2681EA2ABA50F CRC64;

Query Match 79.1%; Score 1077; DB 1; Length 265;  
Best Local Similarity 78.7%; Pred. No. 1.3e-49;  
Matches 210; Conservative 23; Mismatches 32; Indels 2; Gaps 2;

QY 1 MKAAVLT LAVFLTGSOARHFQQDEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGS 60  
Db 1 MKAAVLT LAVFLTGSOARHFQQDD-PQSSWDRVKDFATVYVEAIKDSGRDYVAQFEAS 59  
QY 61 ALGKQLNLKLLDNWDSVTSTFSKLRQLGPGVTQEFWDNLEKETEGLRQEMSKDLEEVKAK 120  
Db 60 ALGKQLNLKLLDNWDTLASTLSKVRQLGPGVTQEFWDNLEKETASTLRQEMHKDLEEVKQK 119

QY 121 VQPYLDDFQKKWQEEEMELYRQKVEPLRAELQEGARQKLHELQEKLSPLGEEMRDRARAHV 180  
Db 120 VQPYLDEFQKKWHEEVEIYRQKVPALGEEFREGARQKQVQLQDKLSPLAQELDRARAHV 179  
QY 181 DALRTHLAPYSDELRLQRLAARLEALKENGGAARLAETHAKATEHLSTLSEKAKPALEDLRQ 240  
Db 180 ETLRQQLAPYSDDLRLQRLTARLEALKKEGGGS-LAEYHAKASEQLKALGEKAKPVLEDLRQ 238

QY 241 GLLPVLESFKVSFLSALEEYTKKLNTQ 267  
Db 239 GLLPVLESFKVSILAAIDEASKKLNAQ 265

RESULT 9  
APOA1\_MESAU STANDARD; PRT; 264 AA.  
ID APOA1\_MESAU STANDARD; PRT; 264 AA.  
AC Q9Z2L4;  
DT 10-MAY-2005 (Rel. 47, Created)  
DT 10-MAY-2005 (Rel. 47, Last sequence update)  
DT 10-MAY-2005 (Rel. 47, Last annotation update)  
DE Apolipoprotein A-I precursor (Apo-AI) (ApoA-I).  
GN Name=APOAI;  
OS Mesocricetus auratus (Golden hamster).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muridae; Cricetidae; Cricetinae; Mesocricetus.  
OX NCBI\_TaxID=10036;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=Syrian; TISSUE=Intestine;  
RX MEDLINE=99061559; PubMed=9843713;  
RA Wu J.Y., Reeves S.K., Wang Y.R., Wu Y., Lei P.P., Lei K.Y.;  
RT "Zinc deficiency decreases plasma level and hepatic mRNA abundance of apolipoprotein A-I in rats and hamsters."  
RL Am. J. Physiol. 275:C1516-C1525(1998).  
CC -!- FUNCTION: Participates in the reverse transport of cholesterol from tissues to the liver for excretion by promoting cholesterol efflux from tissues and by acting as a cofactor for the lecithin cholesterol acyltransferase (LCAT).  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- TISSUE SPECIFICITY: Major protein of plasma HDL, also found in chylomicrons.  
CC -!- SIMILARITY: Belongs to the apolipoprotein A1/A4/E family.

-----  
This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its

CC use as long as its content is in no way modified and this statement is not removed.  
CC -----  
DR EMBL; AF046919; AAC98484.1; -; mRNA.  
DR HSSP; P02647; 1AV1.  
DR InterPro; IPR000074; APOA1\_A4\_E.  
DR PANTHER; PTHR18976; APOA1\_A4\_E; 1.  
DR Pfam; PF01442; Apolipoprotein; 1.  
KW Cholesterol metabolism; HDL; Lipid metabolism; Lipid transport;  
KW Plasma; Repeat; Signal; Steroid metabolism; Transport.  
FT SIGNAL 1 18 By similarity.  
FT PROPEP 19 24 By similarity.  
FT CHAIN 25 264 Apolipoprotein A-I.  
FT REPEAT 67 88 1.  
FT REPEAT 89 110 2.  
FT REPEAT 111 121 3 (half-length).  
FT REPEAT 122 143 4.  
FT REPEAT 144 165 5.  
FT REPEAT 166 187 6.  
FT REPEAT 188 207 7.  
FT REPEAT 208 229 8.  
FT REPEAT 230 240 9 (half-length).  
FT REPEAT 241 264 10.  
FT REGION 67 264 10 X approximate tandem repeats.  
SQ SEQUENCE 264 AA; 30739 MW; 280B23P4C0F0B129 CRC64;

Query Match 74.3%; Score 1012.5; DB 1; Length 264;  
Best Local Similarity 73.0%; Pred. No. 3.4e-46;  
Matches 195; Conservative 30; Mismatches 39; Indels 3; Gaps 2;

QY 1 MKAAVLT LAVFLTGSOARHFQQDEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGS 60  
Db 1 MKTVVLAVAVFLTGSOARHFQORDD-PQTPWDRVKDFATVYVDAVKDSGREYVSQFETS 59  
QY 61 ALGKQLNLKLLDNWDSVTSTFSKLRQLGPGVTQEFWDNLEKETEGLRQEMSKDLEEVKAK 120  
Db 60 ALGKQLNLNLENWDTLGSTVGRQLGPGVTQEFWDNLEKETEWLRREMKNKDLEEVKAK 119

QY 121 VQPYLDDFQKKWQEEEMELYRQKVEPLRAELQEGARQKLHELQEKLSPLGEEMRDRARAHV 180  
Db 120 VQPYLDQFQTKWQEEVALYRQKMEPLGABLRDGAARQKLQELQEKLTPLGEDLRDRMRHV 179  
QY 181 DALRTHLAPYSDELRLQRLAARLEALKENGGAARLAETHAKATEHLSTLSEKAKPALEDLRQ 240  
Db 180 DALRTKMTTPYSDQMRDLAERLAQLKDS--PTLAHYHTKAADHLKAFGEKAKPALEDLRQ 237  
QY 241 GLLPVLESFKVSFLSALEEYTKKLNTQ 267  
Db 238 GLMPVFESFKTRIMSMVEEASKKLNAQ 264

RESULT 10  
APOA1\_TUPGB STANDARD; PRT; 265 AA.  
ID APOA1\_TUPGB STANDARD; PRT; 265 AA.  
AC O18759;  
DT 15-JUL-1998 (Rel. 36, Created)  
DT 15-JUL-1998 (Rel. 36, Last sequence update)  
DT 10-MAY-2005 (Rel. 47, Last annotation update)  
DE Apolipoprotein A-I precursor (Apo-AI) (ApoA-I).  
GN Name=APOA1;  
OS Tupaia glis belangeri (Common tree shrew).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Scandentia; Tupaiidae; Tupaia.  
OX NCBI\_TaxID=37347;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Liver;  
RA Lu X., Chen B., Zhao Y., Wang K., Xue H., Zeng W.;  
RT "Cloning and sequencing of tree shrew apolipoprotein AI cDNA."  
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.  
CC -!- FUNCTION: Participates in the reverse transport of cholesterol from tissues to the liver for excretion by promoting cholesterol efflux from tissues and by acting as a cofactor for the lecithin



```
CC cholesterol acyltransferase (LCAT) (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Major protein of plasma HDL, also found in
CC chylomicrons (By similarity).
CC -!- SIMILARITY: Belongs to the apolipoprotein A1/A4/E family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; AF005638; AAB2326.1; -; mRNA.
CC HSSP; P02647; 1AV1.
CC InterPro; IPR000074; ApoA1_A4_E.
CC PANTHER; PTHR18976; ApoA1_A4_E; 1.
CC Pfam; PF01442; Apolipoprotein_1.
CC Cholesterol metabolism; HDL; Lipid metabolism; Lipid transport;
CC Plasma; Repeat; Signal; Steroid metabolism; Transport.
CC SIGNAL 1 18 By similarity.
CC PROPEP 19 24 By similarity.
CC CHAIN 25 265 Apolipoprotein A-I.
CC REPEAT 67 88 1.
CC REPEAT 89 110 2.
CC REPEAT 111 121 3 (half-length).
CC REPEAT 122 143 4.
CC REPEAT 144 165 5.
CC REPEAT 166 187 6.
CC REPEAT 188 209 7.
CC REPEAT 210 231 8.
CC REPEAT 232 242 9 (half-length).
CC REPEAT 243 265 10.
CC REGION 67 265 10 x approximate tandem repeats.
CC SEQUENCE 265 AA; 30332 MW; 60076BC39FAEA165 CRC64;

Query Match 71.6%; Score 975.5; DB 1; Length 265;
Best Local Similarity 69.7%; Pred. No. 3.1e-44;
Matches 184; Conservative 38; Mismatches 41; Indels 1; Gaps 1;

QY 1 MKAAYLTAVLFLTGSQARHFQQDEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGS 60
Db 1 MKAAYLTAVLFLTGSQARHFQQDE-PQSSWDRVRDLANVYVDVAVKESGREYVSQLEAS 59

QY 61 ALGKQLNLKLLDNWDSVTSTFSKLRELQGPVTQEFWDNLKETEGLRQEMSKDLEEVKAK 120
Db 60 ALGKQLNLKLVNWDTLGSTQKVHEHLGPVAQEFWEKLEKETEELRREINKDLEVDVRQK 119

QY 121 VQPYLDDFQKKQWQEMELYRQKVEPLRAELQEGARQKLHQLHQLSPLGEEMRDRARAHV 180
Db 120 TQPFDELQKKWQEDLERYRQKVEPLSAQLREGARQKLMELQEQVTPPLGEDLSDVRAYA 179

QY 181 DALRTHLAPYSDELRLQRLAARLEALKENGARLAETHAKATEHLSTLSEKAKPALEDLRQ 240
Db 180 DTLRTQLAPYSEQMRKTLGARLEAIKEGGSASLAETHAKASEQLSALGEKAKPVLEDIHQ 239

QY 241 GLLPVLESFKVSFLSALEEYTKKL 264
Db 240 GLMPMWESFKTGVLNVIDEAAKKL 263

RESULT 11
Q8HZ96_9PRIM
ID Q8HZ96_9PRIM PRELIMINARY; PRT; 191 AA.
AC Q8HZ96;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Apolipoprotein A-I (Fragment).
OS Gorilla gorilla (gorilla).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Gorilla.
OX NCBI_TaxID=9593;
```

```
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA O'huigin C., Tichy H., Klein J.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY092008; AAM76625.1; -; Genomic_DNA.
DR HSSP; P02647; 1AV1.
DR SMR; Q8HZ96; 31-191.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0008289; F:lipid binding; IEA.
DR GO; GO:0006869; P:lipid transport; IEA.
DR GO; GO:0042157; P:lipoprotein metabolism; IEA.
DR InterPro; IPR000074; ApoA1_A4_E.
DR Pfam; PF01442; Apolipoprotein_1.
KW Lipoprotein.
FT NON_TER 1 1
FT NON_TER 191 191
SQ SEQUENCE 191 AA; 22087 MW; 2D30919874C8F0F4 CRC64;

Query Match 70.6%; Score 962; DB 2; Length 191;
Best Local Similarity 99.0%; Pred. No. 1.2e-43;
Matches 189; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 38 LATVYVDVLKDSGRDYVSQFEGSALGKQLNLKLLDNWDSVTSTFSKLRELQGPVTQEFWD 97
Db 1 LATVYVDVLKDSGRDYVSQFEGSALGKQLNLKLLDNWDSVTSTFSKLRELQGPVTQEFWD 60

QY 98 NLEKETEGLRQEMSKDLEEVKAKVQPYLDDFQKKQWQEMELYRQKVEPLRAELQEGARQK 157
Db 61 NLEKETEGLRQEMSKDLEEVKAKVQPYLDDFQKKQWQEMELYRQKVEPLRAELQEGARQK 120

QY 158 LHELQEKLSPLGEEMRDRARAHVDALRTHLAPYSDELRLQRLAARLEALKENGARLAETH 217
Db 121 LHELQEKLSPLGEEXRDRARAHVDALRTHLAPYSDELRLQRLAARLEALKENGARLAETH 180

QY 218 AKATEHLSTLS 228
Db 181 AKATEHLSTLS 191

RESULT 12
Q8HZ97_PANTR
ID Q8HZ97_PANTR PRELIMINARY; PRT; 191 AA.
AC Q8HZ97;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Apolipoprotein A-I (Fragment).
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Pan.
OX NCBI_TaxID=9598;

RN [1]
RP NUCLEOTIDE SEQUENCE.
RA O'huigin C., Tichy H., Klein J.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY092007; AAM76624.1; -; Genomic_DNA.
DR HSSP; P02647; 1AV1.
DR SMR; Q8HZ97; 31-191.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0008289; F:lipid binding; IEA.
DR GO; GO:0006869; P:lipid transport; IEA.
DR GO; GO:0042157; P:lipoprotein metabolism; IEA.
DR InterPro; IPR000074; ApoA1_A4_E.
DR Pfam; PF01442; Apolipoprotein_1.
KW Lipoprotein.
FT NON_TER 1 1
FT NON_TER 191 191
SQ SEQUENCE 191 AA; 22087 MW; 2D30919874C8F0F4 CRC64;

Query Match 70.6%; Score 962; DB 2; Length 191;
Best Local Similarity 99.0%; Pred. No. 1.2e-43;
Matches 189; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

Qy	38	LATVYVDVLKDSGRDYVSQFEGSALGKQLNLKLLDNWDSVTSTFSKLREQLGPVTQEFWD	97
Db	1	LATVYVDVLKDSGRDYVSQFEGSALGKQLNLKLLDNWDSVTSTFSKLREQLGPVTQEFWD	60
Qy	98	NLEKETEGLRQEMSKDLEEVKAKVQPYLDDFQKKWQEMELYRQKVEPLRAELQEGARQK	157
Db	61	NLEKETEGLRQEMSKDLEEVKAKVQPYLDDFQKKWQEMELYRQKVEPXRAELQEGARQK	120
Qy	158	LHELQEKLSPLGEEMRDRARAHVDALRTHLAPYSDELQRLAARLEALKENGARLAEYH	217
Db	121	LHELQEKLSPLGEEXRDRARAHVDALRTHLAPYSDELQRLAARLEALKENGARLAEYH	180
Qy	218	AKATEHLSTLS	228
Db	181	AKATEHLSTLS	191
RESULT 13			
Q8HZ95_PONPY			
ID	Q8HZ95_PONPY	PRELIMINARY;	PRT; 191 AA.
AC	Q8HZ95;		
DT	01-MAR-2003	(TrEMBLrel. 23, Created)	
DT	01-MAR-2003	(TrEMBLrel. 23, Last sequence update)	
DT	01-MAR-2004	(TrEMBLrel. 26, Last annotation update)	
DE	Apolipoprotein A-I (Fragment).		
OS	Pongo pygmaeus (Orangutan).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;		
OC	Pongo.		
OX	NCBI_TaxID=9600;		
RN	[1]		
RP	NUCLEOTIDE SEQUENCE.		
RA	O'huigin C., Tichy H., Klein J.;		
RL	Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AY092009; AAM76626.1; -; Genomic_DNA.		
DR	HSSP; P02647; 1AV1.		
DR	SMR; Q8HZ95; 31-191.		
DR	GO; GO:0005576; C:extracellular region; IEA.		
DR	GO; GO:0008289; F:lipid binding; IEA.		
DR	GO; GO:0006869; P:lipid transport; IEA.		
DR	GO; GO:0042157; P:lipoprotein metabolism; IEA.		
DR	InterPro; IPR000074; ApoA1_A4_E.		
DR	Pfam; PF01442; Apolipoprotein; 1.		
KW	Lipoprotein.		
FT	NON_TER	1	1
FT	NON_TER	191	191
SQ	SEQUENCE 191 AA; 22128 MW; D8D0671444C13725 CRC64;		
Query Match 69.5%; Score 947; DB 2; Length 191;			
Best Local Similarity 96.9%; Pred. No. 7.2e-43;			
Matches 185; Conservative 3; Mismatches 3; Indels 0; Gaps 0			
Qy	38	LATVYVDVLKDSGRDYVSQFEGSALGKQLNLKLLDNWDSVTSTFSKLREQLGPVTQEFWD	97
Db	1	LATVYVDVLKDSGRDYVSQFEGSALGKQLNLKLLDNWDSMTSTFSKLREQLGPVTQEFWD	60
Qy	98	NLEKETEGLRQEMSKDLEEVKAKVQPYLDDFQKKWQEMELYRQKVEPLRAELQEGARQK	157
Db	61	NLEKETEGLRQEMSKDLEEVKAKVQPYLDDFQKKWQEMELYRQKVEPXRAELQEGARQK	120
Qy	158	LHELQEKLSPLGEEMRDRARAHVDALRTHLAPYSDELQRLAARLEALKENGARLAEYH	217
Db	121	LHELHEKLSPLGEEXRDRARAHVDALRTHLAPYTDLQRLAARLEALKENGARLAEYH	180
Qy	218	AKATEHLSTLS	228
Db	181	AKASEHLSTLS	191
RESULT 14			
Q8BPD5_MOUSE			
ID	Q8BPD5_MOUSE	PRELIMINARY;	PRT; 264 AA.

AC	Q8BPD5;		
DT	01-MAR-2003	(TReMBLrel. 23, Created)	
DT	01-MAR-2003	(TReMBLrel. 23, Last sequence update)	
DT	01-MAR-2004	(TReMBLrel. 26, Last annotation update)	
DE	Mus musculus 18 days pregnant adult female placenta and extra		
DE	embryonic tissue cDNA, RIKEN full-length enriched library,		
DE	clone:3830418K20 product:apolipoprotein A-I, full insert		
GN	Name=Apoa1;		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;		
OC	Muridae; Murinae; Mus.		
OX	NCBI_TaxID=10090;		
RN	[1]		
RP	NUCLEOTIDE SEQUENCE.		
RC	STRAIN=C57BL/6J; TISSUE=Placenta and extra embryonic tissue;		
RX	MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;		
RA	Carninci P., Hayashizaki Y.;		
RT	"High-efficiency full-length cDNA cloning.";		
RL	Meth. Enzymol. 303:19-44(1999).		
RN	[2]		
RP	NUCLEOTIDE SEQUENCE.		
RC	STRAIN=C57BL/6J; TISSUE=Placenta and extra embryonic tissue;		
RX	MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;		
RA	Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,		
RA	Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,		
RA	Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,		
RA	Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,		
RA	Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,		
RA	Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,		
RA	Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,		
RA	Schrml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,		
RA	Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,		
RA	Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,		
RA	Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,		
RA	Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,		
RA	Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,		
RA	Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,		
RA	Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,		
RA	Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,		
RA	Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,		
RA	Hayashizaki Y.;		
RT	"Functional annotation of a full-length mouse cDNA collection.";		
RL	Nature 409:685-690(2001).		
RN	[3]		
RP	NUCLEOTIDE SEQUENCE.		
RC	STRAIN=C57BL/6J; TISSUE=Placenta and extra embryonic tissue;		
RA	The FANTOM Consortium,		
RA	the RIKEN Genome Exploration Research Group Phase I & II Team;		
RT	"Analysis of the mouse transcriptome based on functional annotation of		
RT	60,770 full-length cDNAs.";		
RL	Nature 420:563-573(2002).		
RN	[4]		
RP	NUCLEOTIDE SEQUENCE.		
RC	STRAIN=C57BL/6J; TISSUE=Placenta and extra embryonic tissue;		
RX	MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;		
RA	Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,		
RA	Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;		
RT	"Normalization and subtraction of cap-trapper-selected cDNAs to		
RT	prepare full-length cDNA libraries for rapid discovery of new genes.";		
RL	Genome Res. 10:1617-1630(2000).		
RN	[5]		
RP	NUCLEOTIDE SEQUENCE.		
RC	STRAIN=C57BL/6J; TISSUE=Placenta and extra embryonic tissue;		
RX	MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;		
RA	Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,		
RA	Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,		
RA	Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,		
RA	Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,		
RA	Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,		
RA	Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,		
RA	Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;		



```
FT REPEAT 111 121 3 (half-length).
FT REPEAT 122 143 4.
FT REPEAT 144 165 5.
FT REPEAT 166 187 6.
FT REPEAT 188 207 7 (incomplete).
FT REPEAT 208 229 8.
FT REPEAT 230 240 9 (half-length).
FT REPEAT 241 264 10.
FT REGION 67 264 10 X approximate tandem repeats.
SQ SEQUENCE 264 AA; 30587 MW; C453FF2019634AAC CRC64;

Query Match 66.4%; Score 904.5; DB 1; Length 264;
Best Local Similarity 65.2%; Pred. No. 1.8e-40;
Matches 174; Conservative 41; Mismatches 49; Indels 3; Gaps 2;

Qy 1 MKA AVLTLAVLFLTGSQARHFQQDEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGS 60
Db ||| :||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 1 MKA VVLAVALVFLTGSQAWHVWQQDE-PQSQWDKVKDFANVYVDAVKDSGRDYVSQFESS 59
Db ||| :||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 61 ALGKQLNLKLLDNWDSVTSTFSKLRQLGPTQEFWDNLEKETEGLRQEMSKDLEEVKAK 120
Db :||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 60 SLGQQLNLNLLENWDTLGSTVSQLQERLGLTRDFWDNLEKETDWRQEMNKDLEEVKQK 119
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 121 VQPYLDDFQKKWQEEEMELYRQKVEPLRAELOEGARQKHLHELQEKLSPLGEEMDRARAHV 180
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 120 VQPYLDEFQKKWKEDVELYRQKVAPLGAELQESARQKQLQELQGRLSPVAEEFDRMRTHV 179
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 181 DALRTHLAPYSDELRLAARLEALKENGGARLAEYHAKATEHLSTLSEKAKPALEDLRQ 240
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 180 DSLRTQLAPHSEQMRRESLAQRILAELKSN--PTLNEYHTRAKTHLKTGKARPAALEDLRH 237
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 241 GLLPVLESFKVSFLSAL E EYTKKLN TQ 267
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 238 SLMPMLETLTKTKAQSVIDKASETLTAQ 264
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Search completed: March 28, 2006, 20:27:32
Job time : 233 secs
```